

**FIGURE 1**

C.CAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATGG**CGTCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCACTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTTCGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTTCTAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAAT  
TGTTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTAAGTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCTTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTGTAA**CCCA**ATGTATCTGTGGGCCTATTCCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902

><subunit 1 of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVLSLENYFSLLNEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-42

#### **Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

#### **N-glycosylation site.**

amino acids 134-138

#### **Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

#### **N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAAGAACCTGAGAAAAC  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT  
GTTCCCTCTTTGGGGGTCTCTACCAGAAGAGGTTCTTGGGGGTGCCCCCTCTGAGGAGGCT  
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTCACTTGTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTGGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT  
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57



**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGCGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG  
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAA

## **FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEI  
RSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAGCCCATTCCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT  
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT  
GCTAGGCCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG  
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
CTGATCAATAATGCTGGTGTTCCTGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA  
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG  
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAAGGCAGTGTGACTCAGCTAACCAACAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAAGAACACATCTCCTTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTTAGA  
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG  
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTT  
AAGTATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 8**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTNLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEPGLFKTNLADPVKVIKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFFFFLKQK
AELANPKAV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCGAATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTTCCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCGGTGCGCACCACT  
 GTAGTCATGTACCCACCGCCGCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTGAGATTGCAGCGGAATATGATTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAAATCCACCCGTCTTACCAG  
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTTCGTACAGAAGACACAA  
 AGACAAATCCAGCGGGGACCACCTCACCTGAGATTAGACCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCTGTGGATCCCCGCCCGGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCAG  
 CTCCCTTCAAGAAGAGCAGAAGTGCCCAACAAGCCTCCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCACTCTGAACATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGA  
 AAGGATACCGCAAGTTTGTCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
 GAGAAAGATTGAGGAAGCCAGGAACTGGGTGTCGAAGAAGTTACACTTTGAAAAGGACG  
 TGGACGTCAACCTGTTTGAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC  
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTAGCTGGAGTTCGGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG  
 GCCTCTTCACCACCTTGGGCGTATTACGCTGGGCGCCAGGGCCGACACTATATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTG  
 TGGGGGAGCTTGCCACGCGCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCAGGA  
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCCGAGATCG  
 TGCACCTCAACCTTTACCCCCAGCCGGGCGTCCGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA  
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC  
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGAGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCTCTGCCTATCT  
 GGACCCCTGCCTAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
 CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCT  
 CTGAAGTGGCTCTGGGCTCCTCCTGCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
 GGCGTCTGCTTGGTGTGATGCGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTTCTCCTC  
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGCAGC  
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC  
 CTGGCCGCCCCGAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGGCCCCCT  
 CCAGTGAATGGGTCTTTTCGTGGAGATAAAAGTTGATTGCTCTAACCGCAA

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## **FIGURE 10**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN
SKSWRRRSCWRKWKQLSRLQRMILFLLAFLLFCGLLFYINLADHWKALAFRLLEEEOQMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEEEAT
KRQEAPVDPREPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPPLPPARTQGTVPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSSTVAEVTSIQLEFRELSRLTGDKKFQEAIVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGEAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GCGCGCGGTAGGCCCCGGGAGGCCGGGCCGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
 CGCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
 AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC  
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCCCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGT  
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA  
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
 CGGGCAGCGCTCATCAACGTGGGCTTCCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCTGAGGCTGGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTTCGGCGGC  
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
 GCCCCCTCGGGAATCACAACCTGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGG  
 AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
 CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
 AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGGTTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
 GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
 GGACCCCCCTGCCTTCTTGCTCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC  
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 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACL SLGFFSLLWLQLSCSGDVARAVR  
GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLV PFRERFEELLVFPVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVG FLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWG WGREDDEFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDQKRIAAQKQE QFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

### **Signal peptide:**

amino acids 1-42

### **Transmembrane domain:**

amino acids 29-49 (type II)

### **N-glycosylation site.**

amino acids 154-158

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

### **Tyrosine kinase phosphorylation site.**

amino acids 226-233

### **N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGGTGCCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCTTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
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## **FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCGAGCGGACAAAG  
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTTCGCCGCTGG  
 GCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
 CTCGCCCCCGCAGGCCCGGCCCGCAGCATGGAGCCACCCGGACGCCGCGGGGCCGCGCGCA  
 GCCGCGCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG  
 GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC  
 AGGGCGGCGGGCGCCGCGAGGGCAAGGTGGTGTGAGCAGCCTGGAACCTCGCGCAGGTCCT  
 GCCCCAGATACTCTGCCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAATCTGGTTC  
 GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTTGCG  
 TCATTACGGTCTTTTGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT  
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
 CACTGCAGGCCCAACAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT  
 GAATTGCCGCTCTTTTACATGACTCCATCTCATCGCCAAGTTGTGTTGAAGGAGACAGCCT  
 TCCTTTCCAGTGATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGTTGATCAGGATG  
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC  
 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTGAGGCTGGATCTACTGGAATTTG  
 GGGCTGTCATGTCCAGACCAACCTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
 AGAGTTCGACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGCGCAGATGTGATAGAGAGGCT  
 TTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAAATGATGTCACTAGAGTTCCTTTAT  
 ATGTTTAATCAGATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAATGGATGTTATATTGTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTATTCAACATATTACCCAAATATTGCTCTGGAAGCTTATGTCATCAAGTCT  
 ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT  
 GCAATGTTTCAAATACATTTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
 AAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
 AAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTTGCTTTGATTCCTTTT  
 CTTACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACT  
 ATTGTTACATGTGAAAAAATTTTATTGACTTAAAAGTTTATTTATTGTTTGTGCTCCT  
 GATTTTAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC  
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTAATCAAGCAAGCTGTAT  
 ATCAAATTTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTAAAAAAAGTATTTCA  
 TTGAAGCAAGCAAAATGAAAGCATTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT  
 GACTACACTGTATTGAAGCAAAATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACCACATT  
 TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG  
 TACTTTATTTCTGTCTTCTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAATGGC  
 TGCATAATAACTGATCCAAACAGGTGTTAGGTGTTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRGRAQPPLLLPLSLLALLLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF  
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
ISNIQAGSTGNWVGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA  
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLN  
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA  
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560

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## **FIGURE 17**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA  
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCA  
AATAAAGGACAGTGGGT CATATAAGTTACTGCTTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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## **FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

**FIGURE 19**

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG  
CCTGGGGTCCCCATGATCGTGGGGTCCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC  
CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCTCCGTGACCCTGATCA  
TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC  
ATCACCTTCGCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCCACCAC  
CTATGTCCAGTTCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCGGCGAG  
ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
CATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
GAGTGCACCAACGTGCTACCCATCCCCCTTCCCAGCTTCTGTTCGGGGCTGGCCTTGCTGTC  
TGTCTCTCTATGCCACCGCCCTTGTCTTCGGCCCCCTTACCAGTTCGATGAGAAGATAG  
GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
TGACCTGGTGCACCTCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
TCCGCCTTTCTCTGTTTTCTCTTCTCTGCTCCCCCTCCCTCCCACCTTTTTCTTTCTTCC  
CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCCCTTTCTTCTGCTGT  
TTCCTTCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT  
CTTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC  
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
TTCCACTCTTCTTTTTTCTCATCTCTTTTTCTGGGTTGCCTGTGCGCTTTCTTATCTGCCTGT  
TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCCTCCA  
CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGCCAGCCGTCCATGCCACAGCCCC  
CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
GTGTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT  
CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCCTTAAATTAAAAAACATATATATATATAT  
ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG  
CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTTGCCAGGCTTACAGAACAC  
CCTAGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCACTATTCT  
CTGTGGTATGAAAAAG

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## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFFVACI  
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFKV

### **Important features:**

#### **Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

#### **N-glycosylation site.**

amino acids 66-69

#### **Glycosaminoglycan attachment site.**

amino acids 18-21



**FIGURE 21**

GAAACGTGCCACCATATGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGT  
CTTGAACTCGTGACCTCATGATCCGCTACTCTCGGCCCTCCCAAAGTGCTGGGATTTACAGGCATGAGCCATGAC  
GCTGGCCAGCCCTATGCATTTTTAAGAAATTTTCTGTATTAGGTGCTGTGCTAAACATTTGGCCACTACAGTGA  
CCAAAAACAGACTGAATTTCCCCAAGAGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAG  
ACCATATTACTCATCTATGACTAAGGTCACAAATGGGGTACGTTGATGAGGAGTGATTTTGTAAAGACTACA  
GAGGGAGGACAGACTACCAAGAGGGGGCCAGGAAAGCTCTCTGCAGAGGTGGTATTTTTCAGCCCAAATCGAA  
GAATGAGAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTACACTACCTTTGGC  
CTGAGAAAAATAGCATGGGATTGGAGGAGGCTGGGGGAACACCACCTTCTGCCGACCTGGGCAGGAGGCATTGAGG  
GCTTGAGAAAGGGCAATGGCAGTAGCAGTAGAAAGCAGAGGTAGGAGCAGGGACTTTGTCAGGTGGAATCATT  
GGTCTTATCAACAGATATGGGCAAGCAAGCCAGGGGAGAATGTATGGTAATGCTGAGGTTTGGAGCCAGGCTGA  
GATGGGACAGTGGTGGGTATGCAAGAGAAAGAGGTCAGGAAGCAGGGCCAGAGCTGGGGAGAAGGTGTGGGG  
TTTGGTTTTCCATCTTGCCGAGCTGTGCCGGAATGTGGATGGGAAGACCAGAGGAGGAGCAAGGGGCCAGAGGGGA  
AGGGAATCTTAAAGAACTCTGGATGCCACATCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTGGTTTCTTCAATTTCTGCTGCCCTGCCCTCCATCTCTCTCTGGTGCTGGGAAAGTGGAGGATAGCTGAAGTTTGT  
CTTCTCGGGGCTGTCTGAATCTCCATTGCTTTCTGGGAGGACATAAATCACCTGTCTCTAGCTTCTTATCATCT  
TACATTTTCCCTGTAGCCATGGGACATATATGTGGTGTTCTTCTCTAGCTCTGTCTCTCTCTCTCTCTCTCTCTCT  
GGTATGGGCATGTTTAGGGGAGAGGTCATTGCTGTGCAGAGGGGCACTGACTTCTAATGGTGTATACCCAAGGTGA  
ATGTTGGAGACACAGTGCAGATGCTGCCCAAGTCCGCGAGGAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCC  
AGGTCTCTCCCTGCATGGTATGCAGCCCCCTCCATGTTTCTGGCCACTTTGTCTTTCTCTCTCCGTTTGCACAT  
CCCCTTTGAACATGTTTCTCTGTGAGTACATGCTGGGGTCTCCCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTTCTCCACCCCAAAGGTTTCACTAGATCTCTAACTACTGCCACCTTCCACTCTCCGACCTGTCTCTCTCTCTCT  
CCTGGTCTTTTACCAGGCTTCTCCACCTCTCCCTATCTCCAGGTATTTCCAGGTGGTGAAGGACCACGTGACC  
AAGCCTACCGCCATGGCCCAGGGCCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCCGAGTGACTC  
ACCTGCTGCCCTGGAATCAGCCTTTTCTCTCTTATTCAGACCTCAGCAGAGGGCGAACAGAGGCTCGCTTTGCAG  
CAGGAGTGGCTGAGCAGTTTGGCATCTCCGGAAGCCAAGTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCC  
ACTGATGACTCTATGATGAGGACTTTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCTTGGGGCC  
GCACCTCAGGACCGTGTTCACCGGCCACCGGTTCTCCCGGCTGTGCGCCAGGGCTCCGTGGAGCTGTAGAGCG  
ACTGCTCAGACAGCGTGTCCCCAGACACCTGTGCTCTAGTGTGTCAGCCTGGAGATGGTGTGGGCTCC  
CCGGCCCGCTGGCCCTCCAGCTGCTGGGCGATGAGCTGCTTCTCGCAAACTGCCCCAGCCGGGAAGGTGC  
CTTCCGAGGCTTGGGCCCACTTGGAGGCCAGGACTACTCTACAACCTGCCCTTCAAGAGTCTGCTCTTCTCC  
CCGGCGAGGAGGAGGCCAGCCCTTCAAGGACTGCCAGCCACTCTGCCACCACTAACGGGCAGCTGGGAACCG  
CAGCGGCAAGCCTCTGACCTGGCTCTTCTGGGGTGGTGTCTTATAGATGAGGATAGGCAGGCCAGAGGAACA  
GTGACCACATCATGCCTGGCAGTGGCATGCATCCCCGGCTGCTGCCAGGGGCAGAGCCTCTGTGCCCAAGTG  
TGGGCTCAAGGCTCCAGCAGAGCTCCACAGCCTAGAGGCTCTCTGGGAGCGCTCGCTCTCTCGGTGTGTGTTT  
TGATGAAAGTGTTTGGAGAGGAGGCGGCTGGGCTGGGGCGCATGCTGCCCCCACTCCCGGGCTTGG  
CGGGGTTTCCCGGGGCTCTGGGGCATGCTACAGCTGTGCGACAGTATGTTTCTTAAATGCCA  
CACACACATTTCTCTCGGATAATGTGAACCACTAAGGGGGTTGTGACTGGGCTGTGTGAGGGTGGGTGGGA  
GGGGGCCAGCAACCCCCCACTCCCCATGCCT  
CAGTGTCTGATAGAAATCACCCCACTTGGAGGGGCTGGCTCTGCTGCCCTCCGGAGCCTATGGGTTAGCGGTCC  
CTCAAGGGCCCCCTGCCAGCTGGGCTCGTGCTGTGCTTATTACCTCTCCATCGTCTCTAAATCTTCTCTTT  
TTTCTTAAAGACAGAGGTTTTTGGTCTGTTTTTTCAGTCCGATCTTCTCTTCTCTGGGAGGCTTTGAATGAT  
GAAAGGCTGTACCTCCACCTTTTCTGGCCCCCTAATGGGGCTGGGCCCTTTCCCAACCCCTCTAGGATG  
TGCGGGCAGTGTGCTGGCGCTCACAGCCAGCCGGCTGCCATTACGACAGAGCTCTGAGCGGGAGGTGGA  
AGAAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTTCTTCTAGAGAGGGCCACAAGAGGGCCACAGG  
GGTGGCCGGGAGTGTGACAGTGATGCTGCTGAGAGCGAGGAATGTGCAAGTGATGACATCATGAGGAGT  
GTCTCTTCTTGGGGAAGAAGAAGTGAAGCTTTCTGTCTGAATGAAGAAGCCAGGCTACAGTACAGGCCCCC  
GCCCCAGCCAGGGTGTTAATGCCACGTAGTGGAGGCTCTGGCAGATCCTGCATTCCAAGGTCACTGGACTGT  
ACGTTTTATGTTGTGGGAGGGTGGGTGGCTTTAGAATTAAAGGGCTTTGTAGCTTTGGCAGGTAAGAGGGC  
CCAAGTTAAGAAGCAGAGGCCAACGGGCCAAGCAAGCAATCTATATAAGTGCTCTATTAGGTGTTTATTTTGTCTT  
ATTAAGAATTTGTTTTTAAATTAATAAAAACTTTGTAATTTCTTAAAA

## **FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLC  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALES  
AFSSYSDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTG  
SWERQRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170,  
228-232, 285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT  
GGCACCTCCTGCTCAGTGCACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCCTTTAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAAAAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA  
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATCCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACATCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAACTCTTTCCAA  
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAGGAAAAC  
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
GATTACGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATCCACCAAAAATTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
TCTTTAAAAGTCTTCAAAGGTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSSSEFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFNTNSKLFNPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA  
MPESEENARDGIPMDDIPPLRTSV

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domain:**

amino acids 235-262

### **N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

**FIGURE 25**

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
CTTAGGCCTTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGGATTCTGAGGATCCTGCA  
AATTCCTTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCTGCA  
CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACTGC  
TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG  
CAAAGTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG  
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTTCAACAAACGTGCCATTGATAA  
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT  
AAGAGGCAACAGATAGAGTGTCTTGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
AAAAAAGGAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAA  
TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG  
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC  
GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG  
GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAATATA  
TCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTTGTAACACTTTCTTGAATTTAGA  
AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG  
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA  
CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF  
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG  
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNNRKSFRLLRRDLLLLGFNKRAIDKCWKIR  
HFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTCGGCGGGAGCACCCAGTCCTGTACGCC  
AAGGAACTGGTCCTGGGGGCACCAATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT  
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
CGCCACCCTGGACCCCGGCCCTCAGCCCACATCGATGGGGCCCCAGCCCACAACCTGGGG  
GGCCCATCACCCCCACCAACTTCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTTG  
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCAG  
GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGACAGCAGTGTCCACCCAG  
TGCTTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTGCGGGCCCCCAAGTGGTCACCTCCCC  
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGCCCTCCCTGTGG  
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
ACAGCTCCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAATACTTTTAAACA  
GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG  
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC  
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
GATCAGGTTGAATGAATGAACTCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
TGTCCACAATATTCGTGAGTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAA  
AAGA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLILLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP  
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPESPACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248



### FIGURE 29

[illegible]

### FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
```

```
><subunit 1 of 1, 440 aa, 1 stop
```

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALCLGSGEAGPLQSGSEESTGTNIGALGHGLGDALSEGVGKAIGKEAGGA  
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGQGNPGLGTPWVHGYPGNSAGSFGM  
 NPQGAPWQGQGNNGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPFPSPGSGGGSSNSGGGS  
 GSQSGSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSSGSSSSGSSSSGSSSSGSSSSGSSSGNSGSSSRGDSGSESSW  
 GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL  
 GSGSDNRYRGQSSWGSGGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQ  
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACC  
 GTGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTT  
 CACTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGCGCAGGAGAGTGAGGGGAAGATGTTTCTTCTGAACA  
 AGCTGCTGCTACTTGTGTCTCTGGGCTGGCTTTTCCAGATTCCCAAGTCCCTGAGGACTTGTCTTTCTGGAA  
 GAGGTCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGA  
 CCAGCAGCTGCTCTACACCTGCTGCCCCACATCGGAGAGCTCCGGAAACTGCTCGCTTCGTGGGTGTCAGGCA  
 GTAGTGGACGGAGTGCGGGCTTCATGAGGAAATCACCCCACTACCAAGCCTGGGAGCCAGCCTTCC  
 CAGACCAGCCAGGGGCTGCAGGCACAGCTCGCCAGGCCTTTTCCACAACCAGCCGCCCTCCTTGCGCCGGAC  
 CGTAGAGTTCGTGGCAGAAAGAATTGGATCAAATGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGG  
 TGCGCCAGGCAGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTG  
 TTGGAGATCTTGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCGTGCAAG  
 GAAGAGCCCTGGGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAAC  
 TTGCTGTGGGGCTTGAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAAATCACAGCACTGATCAGGAGGGAG  
 GTGAAAGCAGCAGTGAGTGCACACTTCGAGCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTG  
 CTCGCCGCCCTGACGTGCTCTTGGCCGTGGGGCCAGGGACCTGACGAGGGAGTCTCCCGAGAGCATCTG  
 GAACAGCTCCTAGGCCAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCCTGTGCCACCTGCTGAGCAGCATCT  
 GGCAAAGTGTCTGTGGAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGT  
 ACAGGCTGGAGAGAGGGCAGGCTCGAAGGCTTCTGCACATGCTGCTTTCCTTGTTGGAAGGAAGACTTTCAGGG  
 CCGGTTCCGCTGCAGCTGCTGCTGAGCCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGA  
 CTTGCTGCTATTCTTGTCTACGGGAGCTGGTGGAGAAGGCTCTGATGGGACGGATGGAGATAGAGGCCTGCCTGG  
 GCAGCCTCCACCAGGCCAGTGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCC  
 GAGCCCCACCTGCCAGAACCCAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCCA  
 GAGCTAGGGCTGAGAAGTGGCCCTGCCTTGGGCATTGCACCAGAACCCTGGACCCCGCCTCACGAGGAGGGCC  
 AAGTGCCCAATGCAGACCCTCACTGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCT  
 ACTGCTGGCATCCACCAAGCGAATCCTAGAGGAAGGAGAGTTGGCTGATTGGGATTTGGCAGAAAGCTC  
 CAGAGATGCCAGTCTGGAGTAGAAGAGGTGGTGTGTTGTTATCTCTTGGATACTAAATGAATGAGGTGTGTG  
 GGCTTGTCAACACAGAAATCAAGCCTCATTTGCTATCCCAGCATCTCTTAAACCTTGTAGTCTTGAATTCAT  
 GACAGAGGCAATGACTCCTGCTTAACTTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTA  
 TCACCAGAGCTGGACTGCCATCTCCTTATAAATGCCATAACACAGGCCGGGTCTGGTGGCTCATGCCCTGTAATC  
 CCAGCACTTTGAGAGGCCTGAGGTGCGCGGACTGCCTGAGGTGAGGAATTCAAGACCAGCCTGGCCAACATGGC  
 AAAACCCCATCTCTACTAAAAATAAAAAATATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCCAGCTACT  
 CAGGAGGATGAGGCAGGAGACCTGCTTGAACCTGGAGGTGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCAC  
 TCCAGTCTGGGTAACAGAGCGAGACTTTCTAGAAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCACTGA  
 AACCTGACTTTCCCTGTACCTTCAGCCCTGTGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGAC  
 CAAGCACAGGGCATTTAGAGCTTTTATAAATAAACTGGTTTCTTTAAAAAAGGGCTTTATTAAATTC  
 TCCCCACAGATGGCTCCTGCAATCTGCCACAGCTCTGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTCCCTG  
 AGGCGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTGGCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTC  
 TTGCCGGGCACAGAGCTGCGGGTCTGGGGGCACCGGAGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGCCT  
 GTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTGGGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGC  
 CGGTGCTCCTTCYTAGGCCAGTCTGGGGAACTAAGCTCGGGCCCTCTTTGCAAGACCGAGGATGGGGTGG  
 GTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGTGAAGAGGGCGCGGTTTGTGGCTGCAGCGGCC  
 TGGAGCCCTCTCTCTGAGCCTCAGTTTCCCTTCCGTCTAATGAAGAACATGCCGTCTCGTGTCTCAGGGC  
 TATTAGGACTTGGCCTCAGGAAGTGGCCTTGACGAGCGTCATGTTATTTTCACAACTGCTCCTGCGACGTTGGC  
 CTGGGCACGTATGGAATGGCCATGTCCCTCTGCTGCGTGGACGTGCGCGTGGGAGTGCAGCAGCCAGAGCGG  
 GGGCAGACGCTGCGCTGGGGTGGGGGAGGGCGCCCCGGGAGGGCTCACAGGAAGTTGGGCTCCCGCACCAC  
 CAGGCAGGGCGGGCTCCCGCGCGCGCCGCCACCAACCGTCCAGGGGCGGGTAGACAAAGTGGAGTCCGCT  
 TGGGCTGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCAGCGCGCTCGTCCGCCAGCTGGAAGCAGCGCCCG  
 TCCACCAGCACGAACAGCCGTGCGCCT

## **FIGURE 32**

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

**FIGURE 33**

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC  
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCTGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAGACACTGCCCTCTCGGTGCCACCACTGTGTGATTGTGAGCAGCTCCAGCCACCTGCT  
 GGGCACCAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCATTC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG  
 CAATTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGGTGT  
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCTATG  
 GCATGGTCCCCCCTAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA  
 TCACCTTCTCCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
 AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCCTTTCCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTGGTGTTG  
 CCCCCTCAATTTCCAGCACCAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGGCC  
 GGCCAGAGAATTTGTGGGGTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGAACAAACCTTCCCCCTCTCTGGG  
 CACCCTTCTGCCCACACAGTTTCCAGTGCGGAGTCTGAGACCCTTTCACCTCCCCCTACAA  
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCCTCCAGCCACTATCCCTTGCTGGAAGGCT  
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTGC  
 GCAAACCTCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT  
 CTAGCAGGGAGGTTTTCCAATGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTCTGCTGGGATGGCTGTGCGGAGCTGT  
 ATCACTGGGTTCTGTCCCTGGCTCTGTATCAGGCACCTTATTAAAGCTGGGCCTCAGTGG  
 GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACCATGAGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC  
 TCCGGAAA

## **FIGURE 34**

MSSNKEQRSADVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCIVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
SSVFRVLRRPQEFVNRTPETVFIFWGPSPKMQKPQGS�VRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRQLQRMPIH  
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPST

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

GTTCTCATAGTTGGCGTCTTCTAAAGGAAAACTAAATGAGGAACTCAGCGGACCGGGAGCGACGCGAGCT  
 TGAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTGTCTGAGGGGCT  
 GGGGCAAGGTGAAAAGTTCAGAACAAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATAC  
 CGTCTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGTCAGGGACGGCAGTATCTCTTTGTGTGACCC  
 TGGCGGCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAG  
 GAATGAGGCCTGAGGTACACATGGCTTGCCCTCTCCAGCCACGACAGGCTGCTTTGTGACTTGAACGAGGTC  
 CCTCAGGTACACCGTCCAGCCTGCGTCCACCGTCCAGGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGGA  
 ACCTCCAAGGATGAATGTAACCTGGCGCCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTC  
 TCATCACCCACGGGACCTCGTCATCACTGCCCTTAACAACCCACACTGTGGGACGGTACCAGTGTGTGGCCCGG  
 ATGCTCGCGGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGT  
 GCAGCAGCTGATTGAAGTGGATGAGGGAAACACAGCAGTCACTGCTGCGCGCTCCACCGTGAAGGCCACCCCAAG  
 CCCAGGTCCGTTACAGCTCAAAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGG  
 AACCTCCAGATTGTGAATGCCAGCCAGGAGGACGAGGGCACTGTACAAGTGTGAGCCTACACCCAGTGACCCA  
 GGAAGTGAACCTCCGGCTCCAGCGACAGGCTACGTGTGCGCGCTCCACCGTGAAGGCTGCCCGCATCATCT  
 ACCCCCCAGAGGCCCAACCATCATCGTCACCAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGGAATC  
 CCACCCCCACGGGTCACTTGGGCCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGGCTTCTCTGCTGAG  
 CAACCTCTCATCGACACCAACAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAAATGGGTGGGC  
 AGCCCCGGGCGAGCGGTCACTCTACAATGTCCAGGTGTTGAACCCCTGAGGTACCATGGAGCTATCCCGAG  
 CTGGTCACTCCCTGGGGCCAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCTCCGTGCTGTG  
 GCTGAGGAATGCTGTGCCCTCATCTCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCCTGCGCGTCCAGCA  
 TGGGGCCTGAGGACGAAGGCGTCTACCAAGTGCATGCCGAGAACGAGGTGGGAGCGCCCATGCCGTAGTCCAG  
 CTGCGGACTCCAGGCCAAGCATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGT  
 ATCACCTTCAAACTCGGCAACCTTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCGACCCCAACGCTCAG  
 TGGGGCCTGCTTCCCCAAGTGTCCAGGAGAGAGGGGCGAGGGGCTCCCGCGAGGCTCCCATCATCTCAGC  
 TCGCCCCGACCTCCAAGACAGACTCATATGAAGTGGTGTGGCGGCTCGGCATGAGGCGAGTGGCCGGGCGCC  
 AATCCTCTACTATGTGGTGAACACCCGACAGCGAGTCAAAAATTCCTTGACGATGGACCTCTCTGGCATTCT  
 CAGCCAACAGCACCGCCTGACCTCACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTAC  
 AACTGTGCGGGAGAGGGCCAGACAGCCATGGTCACCTTCCGAAGTGGACGGGCCAAACCCGAGATCATGGC  
 CAGCAAAGAGCAGCAGATCCAGAGAGACGACCTGGAGGCCAGTCCCGAGAGCAGCAGCCAGCCAGACCAGGCC  
 GCCTCTCCCCCAGAAGCTCCCGACAGGCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGG  
 ATTCCCCGTGGGAATGGTGGGTTCCTTCCAGTCTTCCGTGTGGAGTACAAGAACTGAAGAAAGTGGGAGA  
 CTGGATTCTGGCCACAGCGCATCCCCCATCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCT  
 CCTACAAGTTTCGAGTCCGGGCTCTGAACATGCTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTG  
 GTGTCCGGCTACAGCGTGTGCTGACGAGAGGCGCTGGCAGGTCTTATATCACCTTACCGGATGCGGTGAC  
 TGAGACCAACCATCATGCTCAAGTGGATGTACATCCAGCAAGTAACAACAACCCCAATCCATGGCTTTTATA  
 TCTATTATCGACCCACAGACAGTGAACATGATAGTACTACAAGAAGGATATGGTGAAGGGGACAAGTACTGG  
 CACTCCATCAGCCACCTGCAGCCAGAGACCTCTACGACATTAAAGATGCAGTGTCTCAATGAAGGAGGGGAGAG  
 CGAGTTCAGCAACGTGATGATCTGTGAGACCAAGCTCGGAAGTCTTCTGGCCAGCCTGGTCTGACTGCCACCCC  
 CAACCTGTGGCCCCACACAGCGCCCCCTTCTGAAACCATAGAGCGCGCGTGGGCACTGGGGCCATGGTGGCT  
 CGCTCCAGCGACCTGCCCTATCTGATTGTGGGGTCTGCTGGGCTCCATCGTTCTCATCATCGTCACTTCTCAT  
 CCCCCTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACATACAACAGACCTGGGTTTTCTCGAAGTGCCCTTC  
 CACCTCTCTGCCCGTATATCTATGGTGCCATTGGGAGGACTCCAGGCCACCAGGCCAGTGGACAGCCCTACCTC  
 AGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATGAATAGGGGCTGCCCTCGGCTGCAGTGGGCTA  
 CCCGGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAGCAGCAGAGTGACACCAGCAGCCTGCTGAGGC  
 AGACCATCTTGGCAATGGATATGACCCCCAAAGTACCAGATCACGAGGGGTCCCAAGTCTAGCCCGGACGAG  
 GGCTCTTTCTTATACACACTGCCGACGACTCCACTCACCAGCTGCTGCAGCCCCATCAGCACTGCTGCCAACG  
 CCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAAGGGTGGAGAGGCCCGGACAGTCTGTCTGGAAGCAGTGT  
 GGGACCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCTTGTGCCAGTTGAAGAGGTGGACAGTCTGAC  
 TCCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCGACACCCGTAAGGGGCTACGTAGGACAGGAACCTGGAAT  
 GCAGCTCTCCCGGGGCACTGGTGGCTGTGCTTTTTGAAACACCACTCTCACAATTTAGGCAGAACTGATA  
 TCCCAGAAAGACTATATATTTTGTTTTTTTTTTAAAAAAGAAAGAAAGAGACAGAGAAAATTTGTTATTTA  
 TTTTCTTATATACATATTTATATTTATGCTATGTAATTAATTAATGATATGTTTTATAATTCTGGAGAGA  
 CATAAGGAGTCTTACCGTTGAGGTTGGAGAGGAAAAATAAGAAAGTGCACCTAACAGGAGTCAACAGGAA  
 AGCACCACAGGCTGGCGCGGACAGACTCCTAACCTGGGCGCTCTGCAGTGGCAGGCGAGGCTGCAGGAGGC  
 CCACAGATAAGCTGGCAAGGAGGAGATCCAGGCACATGGTTTCATCAGCAGCATGAGGGAACAGCAAGGGGCA  
 CGGTATCACAGCCTGGAGACACCACACAGATGGCTGGATCCGGTGTACGGGAAACATTTCTTAAGATGCC  
 ATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAGAAACCTTCCAGAATCAATCCGTGGCAACA  
 TATCTCTGTAAAAACAAACACTGTAACCTTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

**FIGURE 36**

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSTGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTI IVTKGQSL  
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGKQGAPEAPI ILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTRGRPKEIMASKEQQIQRDDPGASQSSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT  
 PIHGFYIYYRPTDSDNDSYKKDMVEGDKYWHISISHLQPETSYDIKMQCFNEGGESEFSNM  
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIIVL  
 IIVTFIPFCLWRAWKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTLPPDDSTHQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCCLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879



**FIGURE 37**

CGGGAGGCTGGGTGCTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTTCCCGCGC  
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
CACCCCCAAAACCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT  
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTTACAGACAC  
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
CCGCCTGGGCATGATGATAGATTTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG  
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTTATGACGGGACT  
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT  
TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCTCAGAATGGACACCAGGC  
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT  
CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
TGCT**GAC**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

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## **FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPS  
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT  
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL  
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGNYDGTGRFPQGLEDV  
STYPVLIIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCH  
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-36

#### **Transmembrane domain:**

amino acids 313-331

#### **N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

#### **N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCATG  
AAGCTCTTATCTTTGGTGGCTGTGGTCCGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA  
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
CACCACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGTGGCCTGTTGCTCT  
ACATGGCCTTCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
GGGACCCCGAGCAAAACAGTCTTGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGATGGGCTGG  
TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTCCTCCTT  
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGA  
ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA  
GGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTACAGCATGTGTTCTTTCTGCAGTG  
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGA  
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC  
CACAGTCACTGAGCCAGACGGTCCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
CACCACAGCCCCCTGTACTTGGGTGTCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA  
GAGAAAATTTGTCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTG  
TTTTATTTCTCTCA

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## **FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM  
PVPGHDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE  
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 90-112

#### **N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCCCG  
 AACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGACCCCAAGTGAGGGGCCCCGTGTTGGGGTCTCTC  
 CCTCCCTTTGCATTCCCAACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCCCTCGCCGGGAGATGGCCGCGTTG  
 ATGCGGAGCAAGGATTCGTCTGCTGCTGCTCTACTGGCCGCGGTGCTGATGGTGAGAGCTCACAGATCGG  
 CAGTTTCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAAGCCGCCAATCGAT  
 CTGCGGGCATGTACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGT  
 AGCAGTGATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTG  
 TCGGAGAAAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTA  
 TCCCAGTTACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAC  
 GGTCACTTACTCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGG  
 GCATGAAGGAGACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTCTGGACCA  
 AAATCTGCAAACAGTGTCTCCATCAGGGGGAAGTCTGTACCAAACAACGCAAGAAGGGTTCTCATGGGCTGGAA  
 ATTTTCCAGCGTTGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGC  
 CAGACTCCATGTGTGTCAGAAAAATTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTAT  
 TTAATGCATTATAGCATGGTGGAAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAAATAAGAAACGTGATAAGAA  
 TATAGATGATCACAAAAAGGGAGAAAGAAAAACATGAATGAAATAGATTAGAATGGGTGACAAATGCAGTGCAGC  
 CAGTGTTCATTATGCAACTTGTCTATGTAAATAATGTACACATTGTGGAAGATGCTATTATTAAGAGAAACA  
 AGCACACAGTGGAAAAATTACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTC  
 CTTCAGATTGCTGATTGCTTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATA  
 CTCTAGATAAATTGTTTATACAAATAGGTTCTAAAAATAAAATTTGCTAAACAAGAAATGAAAAATGAGGACATT  
 GTTAATTTACAACAGAAAAATTACCTTTTGATTTGTAACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGAT  
 AAGAAAAAATCAGTCAATATTTCCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGA  
 CAAATAAATAACAAACAAACAGCCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAAC  
 TGATACAAGACAAAAACAGTTTCCTTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCTCT  
 GCTCTGAATGCATTATATTTTCCAACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAAATT  
 TTCACAGATGGCAAAAAATTTAAAGATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCT  
 TAAAGATTGGCCATAACCTATATTTTGTATAGAATTAGATTGGTAAATACATGTATTTCATACATACTCTGTGGTA  
 ATAGAGACTTAAGCTGGATCTGTACTGCACTGGAGTAAGCAAGAAAAATTGGGAAAACTTTTTCTGTTTGTTCAGG  
 TTTTGGCAACACATAGATCATATGTCTGAGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTC  
 TAAATGAATATCTGCATGGGATTTGCTATCATAATATTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCT  
 CGTACTATCCTCAAATTATTTATTTTATAGTGCTGAGATCCTCAAATAATCTCAATTTTCAGGAGGTTTCACAAA  
 ATGTACTCCTGAAGTAGACAGAGTAGTGAGGTTTCATTGCCCTCTATAAGCTTCTGACTAGCCATGGCATCAT  
 CCAATTTTCTTCCCAACCTCTGCAGCATCTGCTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTG  
 CGGTTAAAAAATAAAGTAGGATAACTTGTAACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAAT  
 TCTTTGAAACCACTTTACTACTTTTTTTAACTTAACTCAGTTCTAAATACTTTGTCTGGAGCACAAAAACAATA  
 AAAGGTTTATCTTATAGTCGTGACTTTAACTTTTGTAGACCACAATTCACTTTTGTAGTTTCTTTTACTTAAAT  
 CCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAGAGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTTCA  
 ACTTCCACATATATTTACTAAGATGATTAAGACTTACATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAA  
 ACTAGTCCATCCAAGAACCAGGTTTGTATAAACAGGTTGCTATAAGCTTGTGAAATGAAATGGAACATTTTCA  
 ATCAAACATTTCTATATAACAATTATTATATTACAAATTTGGTTTCTGCAATTTTTCTTATGTCCACCCTT  
 TTAAAAATTTATTTTGAAGTAATTTATTTACAGGAAATGTTAATGAGATGATTTTCTTATAGAGATATTTCT  
 TACAGAAAGCTTTGTAGCAGAAATATTTTGCAGCTATTGACTTTGTAATTTAGGAAAAATGTATAATAAGATAA  
 AATCTATTAATTTTTTCTCTCTAAAAACTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRC  
NN  
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCGTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA  
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT  
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT  
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCAACCACCAAAAATGGCAAACA  
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC  
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCCT  
CCTGGTTTGGAGTCCTTTCTTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG  
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
AAAATAGTAATCAGATTCCCATCAGCTTGTATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA  
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG  
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC  
AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
TGTGGAAAACACCAGTTGGTCAATGGCTCATTGCTTAAAAAAGCAGCCCTTTTGCTTTTTTGT  
TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC  
TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG  
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
GTCTGAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDSKYSSKLLLSWLVPKQKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24



**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTGCT  
TTGGAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
GTCCGCCTGGAGGTCAACGACGGCCCCCGGCCACCCCCGCCTACTGGGACGGCGAGAAGGA  
GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT  
GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACTGGGACCGGCAGCCGCCCCGGG  
GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCGCGCCTA  
CGGGCCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC  
CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC  
GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCCAG  
ACCCACACTGGCGCGCGGCCACAACGTCAATGTCAATGTCATCGTCCCCGAGAGCCGAGCCCAC  
TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC  
TGTCTCCTGGCGCGCCGCGAGGCGCCGCGGAGGCTACGAATACTCGGACGAGAAGTCGGGAA  
AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  
GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCCTTTTCT  
GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAAC  
AAAATCCCACTGATGCCCATCATGCCCTCAGACCCCTTCTGGGCTCTGCCCGCTGGGGGCCTG  
AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA  
GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT  
GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT  
GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA  
AAAAA

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## **FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLLDL  
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEP PPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPLPAKYIDL DKGFRKENCK

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTT  
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
ACTGCTTGAGAAGCTGCTGGACCGCCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT  
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT  
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCG  
TGCCCTCCATGCTGTGCGCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
CGTGTCTCTGGCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
GGTGGACACTTCTCTCGGACCCGTGGTTTTTTTTTGCGGTCAACATTGTCTGCATGGTGATCC  
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG  
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
GCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC  
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACCTTTGCTGACCTAT  
GTGGCCGGCAGCTCACC GCCTGGATCCAGGTGCCAGGGCCCCAACAGCAAGGCGCTCCCAGGG  
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACACCAGCCCCGCGT  
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCGCACTCCTCAGCTCCCTGTG  
GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGGG  
CTCAGCCTGCTCTACCCTCCTGGTGACCTCATCTAGAAGGGAGGACACAAGGACATTGGTG  
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCAGTCATATTAACAGAACT  
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA  
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCT  
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
AGTCCCCTGGCATGGTCAGTCCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
GCGGGTGAACAACCTGCCCCTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT  
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
GTATTCAAAAA

**FIGURE 48**

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLA AHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472



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## **FIGURE 50**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVLLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCA  
**TG**GACGCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGG  
AAGAACTCAGAGCCGGGAAGCCCCCATTCAGTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTT  
CCTGCTGTCTGTTACAAAGATGCTTTTATCTTTAACTTTTGTGTTTTCCCACTTCCGACCCCGGCGTGTATCT  
GCATCCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGAC  
CTGAACAATCAGTCTGTGGGAATTGAGGGAGGAGCAGGAAGGGGGTTTCCAGAAAGAAATGACCTAACAAG  
TTGCTGCTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCT  
GCTTGGGATATAGAAAACCAACCAGCCCTACAGCTGGCTATCTTACAAACAGGTGTCTGATAGAGCAGTATC  
CTGGGTTCTGTCTCTTGCAATAAGGTTATAAATCATCACCAGACAGTTTGTCTGGCATCTTTGCTCAGAATAG  
GCCAGAGTGGATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGG  
GACCAGAAGCCATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCA  
TTGGTGCTGATAGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGA  
TGATGACCTGAAGCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCA  
AAGAGCACTTCAGAAAACCTGTGCCTCTAGCCCAGAAAGCCTGAGCGTCATCTGCTTCAACAGTGGGACCACA  
TGAGGCCAAGACACCCTTGAAGAAGTTCTTGTGAAGCTGGCTGTTTTCAATGCTGCTGCCTTCTCAAATGTGTGGA  
GCATGCTTATGAGCCACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTG  
TACAGGCTGTTGTGTACAGCTGTGGAGCCAGAGTTGGATTCTTCAAGGGGATATTGGTGTCTGGCTGACGAC  
ATGAAGACTTTGAAGCCACATTGTTTTCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAA  
TGAGGCCAAGACACCCTTGAAGAAGTTCTTGTGAAGCTGGCTGTTTTCAATGCTGCTGCCTTCTCAAATGTGTGGA  
GTATCATCAGGCATGATAGTTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTT  
CGTGTAAATTGTCACTGGAGCTGCCCCCATGTCCACTTCAGTCATGACATTTCTCCGGGCAGCAATGGGATGTCA  
GGTGTATGAAGCTTATGGTCAAACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAG  
GTCACGTTGGGGTGCCCTGGCTTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAGTG  
AATAATGAAGGAGAGGTCTGCATCAAGGGTACAACCGTGTTCAAAGGATACCTGAAGGACCTTGAGAAGACACA  
GGAAGCCCTGGACAGTGTGGCTGGCTTCACACAGGAGACATTGGTCTGGCTCCCGAATGGAACCTCTGAAGA  
TCATCGACCGTAAAAAGAACATTTTCAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATC  
TACAACAGGAGTCAACAGTGTTTACAAATTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGT  
GGTTCTTGACACAGATGTAATCTCCCTCATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCC  
AAAACCAAGTTGTAAGGGAAGCCATTTTAGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTT  
GAACAGGTCAAAGCCATTTTCTTCATCCAGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAA  
AGCAAAGCGAGGAGAGCTTTCCAAATACTTTTCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAGG**  
ATAAGGTACTTAAGTACCTGCCGGCCCACTGTGCACTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATT  
TGTTTTGCTTTTCTCTCATTTTTTTTTTAACTGTTAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACA  
TATAATGTGTAACTTAGTTCACAAATAAATCAATCCTGTCTTTCCCATCTTCGATGTGCTAATATTAAGGCT  
TCAGGGCTACTTTTATCAACATGCCTGTCTTCAAGATCCCAGTTTATGTTCTGTGTCTTCTCATGATTTCCA  
ACCTTAATACTATTAGTAACCACAAGTTCAAGGGTCAAAGGGACCCTCTGTGCCTTCTCTTTGTTTTGTGATA  
AACATAACTTGCCAACAGTCTCTATGCTTATTTACATCTTCTACTGTTCAAACCTAAGAGATTTTTAAATCTGA  
AAAAGTGTACAATTATGTTTTCTAGCCACTCCACAAACCACTAAAATTTAGTTTTAGCCTATCACTCATG  
TCAATCATATCTATGAGACAAATGTCTCCGATGCTCTTCTGCGTAAATTAATTTGTGTACTGAAGGGAAAAGTT  
TGATCATACCAAACATTTCTTAACTCTCTAGTTAGATATCTGACTTGGGAGTATTAATAATGGGTCTATGAC  
ATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATATTACAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACA  
GTTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACAGGTGGGCCAGTGAACCTTTCCAGTAAATGAAG  
CAAGCACTGAATAAAAACCTCCTGAACCTGGGAACAAAGATCTACAGGCAAGCAAGATGCCACACAACAGGCTT  
ATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGGATTAGAGTTCTGTCTACCTTACCCACAGATAA  
CATATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAACTATTACAGATAAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN  
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
PDQFVGIFAQNRPEWIISELACYTYSMAVAPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ  
AVVYSCGARVGFFQGDIRLLADDMLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
SQPVLQIFVHGESLRSSLVGVVVPDTPDLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI  
GKESGLKTFEQVKAIFLHPEPFSEIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622



**FIGURE 53**

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG  
 CCGGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGGCCGTGCTTTTCCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGACGTAGA  
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGTCTGGAGGATG  
 AGGCCCGGGAGCAGGGCCGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTT  
 CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCAATGTCAG  
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCT  
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCCTTGTAACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCTTGACG  
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACGAGGCC  
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTTGTTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTGCAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCCTCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCCTGGTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC  
 ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
**ATG**AGACCTCCTCCAGGACCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA  
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGAGTT  
 AAAAGTCTATTTATTTACTTCCTTGTTGGAGAAGGGCAGGAGGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCAGGCCTGGCTCAGAATCTA  
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTTA  
 GACACTGGACAGGCCTCCTCTCAGCCTTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT  
 GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAA

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## **FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVNIKLILDTR  
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK  
DTAKALLRSLGSQAGPALGWRDWTWAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS  
AEEAECHWADTELNRNRRRRFCCKVEGYGSGVCSCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY  
KASLTATFNLFPEAKFAVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
EDPALLYRVETMPGLGWVLRRLYKEELEPKWPTPEKLWDWDMWMMPEQRRGRECIIPDVS  
RSYHFGIVGLNMNGYFHEAYFKKHKFNTPVPGVQLRNVDLKKKEAYEVEVHRLLEAEVLDHS  
KNPCEDSFLPDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLVDVRGNHRGLWRLFRKKNH  
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACA  
 CCTGTTTTAAAGAACCTAAGCACCATTTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAA  
 TAAAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATG  
 TTACGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTT  
 TTGGGTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCATCGTGCCCTGAAGGAGTACATGCCCTTT  
 ATGAAGATATTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAA  
 AGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTAT  
 ATTGGTGTTCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATG  
 TGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAATCACCACCACGCTGGGTCT  
 GGTGTGTCATGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTC  
 CAGTTAATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCT  
 TGATGCATGCTGGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACC  
 AGTTATGTCCATGGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAGCCCTTTTCAGAGGTGAAC  
 GCCACGGGAGTGGCCATGCTTTTCTGCGGGGACATTTCTTTATGTTGCCACAGTACATGTCTCTCC  
 CTGAGGTGGGCGGAATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCT  
 GGAAGTGGCAGCCCTGTTCTGGGTTGCCTCATCCCTCTCATCCTGTGCTAGTAGGACACCAGCATTA  
 ATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCAGTGACAGC  
 TACTCACTTCCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCAGAGGGG  
 AGGTGAGGTTAAACCTGAGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGC  
 TATAGACATCCCATTGTGTTATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAAATATTTCTCTTAA  
 CCTATTCTCAGGGAAGATGGAATTTAGTTTAAAGGAAAAGAGGAGAACTTCATACTCACAATGAAA  
 TAGTGATTATGAAAATACAGTGTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCT  
 GCTACTTTATCCATTGATTTTAAACATGGTTCCACCATGTAAGACTGGTGTCTTAGCATCTATGCC  
 ACATGCGTTGATGGAAGGTATAGCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGG  
 GATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCA  
 TTGAAAAGGGATGTCTAGAGGGATTTAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGC  
 CATTCATCAAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCAT  
 TCCTTGTCAAGTTCTCCTTTGCAGAATACCTGTCTCCACATTCTAGAGAGGAGCCAAGTTCTAGTA  
 GTTTTCAGTTCTAGGCTTTCTTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATAT  
 TAAATTTTAAAGTGATTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAA  
 AATGTATGGTTGTCTTTTTTTTTTGTTTTTTTTTTTTTTAAATTATTTCTCTTAGCAGATCAGCAATC  
 CCTCTAGGGACCTAAATACTAGGTCAGCTTTGGCGACACTGTGTCTTCTCACATAACCACCTGTAGC  
 AAGATGGATCATAAATGAGAAGTGTTTGCCATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCT  
 TCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTTTCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCT  
 TACTGCTGGTGTAAATATTTGTGTGGGATGAATTCCTATCAGGACAACCATTCTCGAACTGTAATA  
 ATGAAGATAATAATATCTTTATTTCTTTATCCCCTTCAAAGAAATTACCTTTGTGTCAAATGCCGCTT  
 TGTTGAGCCCTTAAATAACACCTCCTCATGTGTAAATTGACACAATCACTAATCTGGTAATTTAA  
 CAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATAATTTTTTTTTTCAATTTGCCCCAAATTTTGT  
 TAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTACTTTCTATACCAT  
 TTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTTTCTTCAGGGCAGTGGACGTAGTAGTTTG  
 TAAAAACGTTTCTATGACGCATAAGCTAGCATGCCTATGATTTATTTCTTTCATGAATTTGTCACT  
 GGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAA  
 TAGGATACAGTTGTATGTAGTCATTGGCAACAATTCATACAATTTTACTACCAAGAGAAGGTATAG  
 TATGGAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCTGACTGGTGTGAGACTTGAGGTTTC  
 ATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTGGAACCTGACTTTGTCAAATAAATAG  
 CAGATTGTAGTGTCAAAAAA

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## **FIGURE 56**

MDDFISISLLSLAMLVGCYVAGI I PLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSDHTQLHAYIGVSLVLGFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHL LVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

**FIGURE 57**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
GAAACGGGCGTCCGAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT  
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA  
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA  
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAA  
GTCCCAGACACCAGCCCCAGTTCCGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA  
TAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATC  
TGA

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## **FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQQLQALSEPQPRLQAAGLPHTVEVPQGKGNVLGNSKSQTPAPSSEVVLSKR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

**FIGURE 59**

GGATGCAGAAAGCCTCAGTGTGCTCTTCCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTC  
 ACCAGTGGCTTCTGCTCACCCGTTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTC  
 CCTGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGC  
 TGATAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTCACACGTGCTTAGAGAGCCTCTGTCTCCCTA  
 CCCTTCCTGGGCAAACCTAAGCTCCTTGACAGAGATCCTGGAGATTACGCCCCACCATGCCCGCTCTACCGATC  
 TCAGGTTGACCCTCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCACTGGCTCACTGCCTACCTTTATTG  
 ATGCTGGTAGTAACCTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCACTGCAGGAAGG  
 CGTGTAGTCTTCATGGGAGATGATACCTGGAAGACCTTTTCCCTGGTGCTTCTCCAAAGCTTTCTTCTTCCC  
 ATCCTTCAATGTACAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCCCACCATGGACAGTG  
 GTGAATGGGACGTGCTGATGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACTCT  
 GAAATGGCCAAAGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACT  
 GCTGGTAGTGGCTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAG  
 CTGCTCTCTTTCTGTATAGCCCCACAGCAGTCTTCCCCAGCACCCCCACAGAGGAGCCAGAGGTGATTCCTCAA  
 GTTAGCCTTGTGCCACGCTGGCCCTGCTGCTGGGCCTGCCCATCCATTGGGAATATCGGGGAAGTGATGGC  
 TGAGCTATTCTCAGGGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCA  
 ATGCTCAGCAGGTGTCCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAAGCTAAGGAGCTTCAT  
 CAGCTGCAGAACCTCTTCTCCAAGGCCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGC  
 GACACTGCCGACTGTGATTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGG  
 CTGTTTTCTCTGTGTCCGATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCTGTGGCA  
 TCTCAGTGGGCAATATCCCCAGGCTTTCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGG  
 GGCCATAGCGTATGCTGGACTCCTGGGAATATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTG  
 CAGTGAGCTCATTCCTCCCTTTTCTGTGAAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCCCTGGCAACCCTG  
 TTTCCATCCCTGGGCCGCTCCTGTTACTCCTGTGTTTCGTTGGCTGTGTTCTTCTGTATAGTTTTTGTGTG  
 AGCTGAGGCCAGGGCCACCCCTTCTTTTGGGCTCATTCATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGG  
 GCCAGCTGCTTCCACCTAAGCTACTACAATGCCCCGCTTGGCACTTCAGCCACAACAAACCCCCACGGCAC  
 AATGGTGCATATGCCCTGAGGCTTGAATGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTATCGTTG  
 CCCTGAAGAGACACCTGTTTGGCACTCCTCTCCCTGGCTGAGTCCCTCTGGCATCCATGGTGGGTGGTCGAGCCA  
 AGAATTTATGGTATGGAGCTTGTGTGGCGGCGCTGGTGGCCCTGTAGCTGCCGTGCGCTTGTGGCTTCGCCGC  
 TATGGTAATCTCAAGAGCCCCGAGCCACCCATGCTCTTTGTGCGCTGGGGACTGCCCTAATGGCATTTGGGTAC  
 TGCTGCCTACTGGGCATTGGCGTGGGGGCGAGATGAGGCTCCCCCGCTCTCCGGTCTCTGGGGCAT  
 CCATGGTGTGCTCGGGCTGTAGCAGGGCTGGCTGCTTCAGGGCTCGCGTGTGCTCTGGAAGCCTGTGACA  
 GTGCTGGTGAAGGCTGGGGCAGGCGCTCCAAGGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTC  
 TCAAGCTGACTTGGATTATGTGGTCCCTCAAATCTACCGACACATGCAGGAGGAGTTCGGGGCCGGTTAGAGA  
 GGACCAAATCTCAGGGTCCCTGACTGTGGCTGCTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACA  
 GCCCTCACCTGTTGGCTTCCCACTTCTGCTGTTGCATGCGGAGCGCATCAGCCTTGTGTTCTGTCTTCTGTT  
 TCTGCAGAGCTTCCTTCTCCTACATCTGCTTGTGCTGGGATACCCGTACCAACCCCTGGTCTTTTACTGTGC  
 CATGGCAGGCACTCTCGGCTTGGGCCCTCATGGCCACACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTT  
 CCAGCCATCCATTGGCATGCAGCCTTCTGTGGGATTCCAGAGGGTTCATGGCTCCTGTACTTGGCTGCCTGCTTT  
 GCTAGTGGGAGCCAACACCTTTGCCTCCCACCTCCTCTTTCAGTAGGTTGCCACTGCTCCTGCTCTGGCCTT  
 TCCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGCCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCC  
 GAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGGATGCGCCTCAGCACTTCTATGCAGCACTGCTGCA  
 GCTGGCCCTCAAGTACCTCTTATCCTTGGTATTAGATTCTGGCCTGTGCTTGGCAGCCTCCATCCTTGCBA  
 GGCATCTCATGGTCTGGAAAGTGTTTGCCCTAAGTTATATTTAGGCTGTGGGCTTCATTGTGAGCAGCGTG  
 GGAATCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTGTGTGAGCTCCTGGTTCAGGCAGCTATTCTC  
 GGCCACGAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCTACAGAGAGTGTGGAGAACAGTGTAGCCTG  
 GCCTGTACAGTACTGGATGATCTGCAAGACAGGCTCAGCCATACCTTACTACTGCAGCCAGGGGCGCGTG  
 ACATCTAGGACTTCATTATTCTATAATTCAGGACCACAGTGGAGTATGATCCCTAACTCCTGATTGGATGCAT  
 CTGAGGGACAAGGGGGGCGCTCCGAAGTGAATAAAATAGGCCGGGCGTGGTGAATGACCTATAATCCCA  
 GCACCTTGGGAGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCAAGACCAGCCTGTGGAACATAACAAGA  
 CCCCCTCTACTATTTAAAAAAAAGTGAATAAAATGATAATAT

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## **FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQKPGACW  
MASRFSRVVLVLIDALRFDAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ  
VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF  
PGAFSKAFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHPHEM  
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPST  
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAEFSGGEDSQPHSSALAAQASALHLNAQ  
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPCPLLLTPVAWGLVGAIA  
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA  
VFFSDSFVVAEARATPFLGSEFILLVVLQHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY  
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA  
AVRLWLRRYGNLKSPEPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVL  
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
LLHLLAAGIPVTTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS  
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQOPPGNEADARVRPEEEEEP  
LMEMLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG  
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

#### **Leucine zipper pattern.**

amino acids 843-864

#### **N-glycosylation sites.**

amino acids 37-40, 268-271



**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT  
GTCTCTGGTGGTTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
TCATCACAAATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
CCTGACAGCTCCAGAGAAGTGGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA  
GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCCCTCAATATCTCGGATGAT  
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA  
ATATGATGTGAGAACCCTGACATTTGTGCGGGGCTGAAAGAGCAGGAGCTCAGTTTGCAGG  
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCC  
CAAACGTTACAGTACTCATAACCCCCTCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCA  
CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCTGACTGGGATCCCC  
AAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
TATATGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC  
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT  
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG  
TGGGTGT

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## **FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED  
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTTDICAGPEEQELSL  
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTACCAACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
CCGACGCTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCCCTGCCTGGGACCAACAGGCCCCCAGGAGAAGCCGCCTGAGCCACAACCT  
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAAATGTTAAGTACAAAAAAAAAAAAAAAAAAAAAGAAA

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## **FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHC  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**

amino acids 1-30

**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCCGGCGCTGGGCACGGTAG  
 CAGGCGCCGCGCTGTGCTCAAGGACTATGTACCCGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT  
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCCTCCCCAGAT**TA**ACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGGCCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTCCGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCCTCTCTGAGCCTTGTTTCTTTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTGAGGGCTTCCCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC  
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA  
 TTGCCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAC  
 TTGCTCATTT

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## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN  
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD  
LNNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARLW  
AESARLVGLEAPSVREQPLPR

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGCA**ATGT**GGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCGAT  
 GAGGATTCAACAACCCCTGTGGCTAACCCTCTGCTTGCAATTTACTCTCATCAAACGCCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTCAGACCCCTGGGTTCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT  
 GAGACCAATTCCACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCTCAA  
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGTCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTGCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC  
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG  
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC  
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
 ATGTTTATAAATCAAAA

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## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAI PWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDITYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19



**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
CGCCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT  
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAAACCCCTGAAAGTGCCTTCC  
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTATGTTTATGGTCTCCTTCATTGGT  
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTTGGGAT  
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA  
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACCTATCGAC  
AAGGAGCGTTTTAGTGTGCAGGATGTATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
CTGGTTCATGGACAACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG  
ATGCTGCTTGTGCTACCCCAATTAGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGGCCCTCTGCCACACA  
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT  
GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA  
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG  
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC  
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA  
GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTAA  
TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

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## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL  
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGV PYTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV IIFMDNYTIMACILLGILLPQFLG  
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC  
TTGATCCAAGCCACCCTCAGTCCCACCTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA  
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA  
TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC  
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT  
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTTCAGCCTCATCGTGAGTCA  
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG  
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA  
GTGAAGCCCTCCGCCCTTTGTTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
AGCCTCCTTGTTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
CAATAAACACTTGCCTGTGAAAAA

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## **FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM  
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL  
GAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAABAVALSPEEFMVLLDSVL  
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL  
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL  
LPNQNGKLRSGLVPVSLVKALGFEEAESSLTkdALVLTpASLWKpSSPVsQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

**FIGURE 73**

GAGCGAACATGGCGAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAACCTGCATAGACAGTGTGTGCTTTGCAAGCAAGCTGATGAAGAATTCAGATCCTGGC  
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCATGGTGGATTTTG  
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT  
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
 TGAGCAGATTGCCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
 GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGTCTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGTTAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC  
 CTCTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTA  
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC  
 TGTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCTTTTGGAGTAGAGAAATTATGTGTGTGTCATGTGGTCTTCTGAAAATG  
 GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA  
 GATTTTCAGATTCAATCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA  
 TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTCAGGAGTTGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCCTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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## **FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMWETNKRVPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLMGVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

### FIGURE 75

[illegible]

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## **FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF  
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLI RNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHTDAIKIPKWSPLS  
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
SSDHGELAMEHRQFYKMSMYEASAHVPLLMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS  
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSI INYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAIDQWLKTHMNPRAV

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416, 498-501

#### **Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97



**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG  
GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGTGCCAGCATTGTGACAG  
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
TGTGACATCTATAGCACCTTCTGGGCCTGCCCCGTGACATCCAGGCTGCCCAGGCCATGAT  
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
ATCCTTGGAGGCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC  
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
ATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
CACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGTGTGAGAAGGTGCTGCTGAGG  
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG  
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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## **FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRICTVFCQESRAKDRVAVAGGVF  
FILGGLLGFIPVAWNLHGILRDFYSPPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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## **FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG  
TGAAGCTGAAGGTTTCAGGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCCCTTGAGAAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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**FIGURE 80**

MVPRI FAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

**FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA  
CTCAGCCCCGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGGAACCCCTCACCCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

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## **FIGURE 82**

MAPRGCI VAVFAIFCISRL L CSHGAPVAPMTPYLM L CQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDR L CRSVS

**Signal peptide:**

amino acids 1-24

**FIGURE 83**

GGGGGCGGGTGCTGGAGCACGGCGCTGGGGCCGCCGAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCTCCCGCCGCTCCCCGGCACCAGAAGTTCTCT  
 GCGCGTCCGACGGCGACATGGGGCTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC  
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGAGAACGTCAACCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACGACCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCCGTGCCCAGGAGCTGGTGCAGGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTTGAAGCCTCACCACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGACCCCCCTG  
 TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTTCGAGGCCAGCAC  
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCCTGTCCCTGACT  
 CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG  
 ATTCTCCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCCGTGGCCGCTTGGCTCCCCCGTTTTGGCCGAGGCTGCTCTTCTGTCTC  
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCCTGGCCATCGCC  
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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## **FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTCRLGPDVK  
GHDVTFYKWTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216



**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC  
TTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG  
GGTCTGTGGGTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGA  
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCCGAGGTGAGGGTCCTC  
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCCGCC  
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACT  
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG  
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC  
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC  
CGCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC  
CCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
GCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
AAGACGTA CTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG  
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA  
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCT  
CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
CCTCGGACTTGTTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG  
AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGA  
CAAAGTGACCAAGACATAACAAAGACCTTAAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 86**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHYPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTPEQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

Year	United States (%)	Japan (%)	Germany (%)
1950	7	7	15
1960	8	8	16
1970	9	10	17
1980	10	13	17
1990	11	16	17
2000	12	18	17
2010	13	19	17
2020	14	20	17
2030	14.5	20	17.5
2040	15	20	18
2050	15	20	18

**FIGURE 87**

[illegible]

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## **FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

**Signal peptide:**

amino acids 1-18

**FIGURE 89**

[illegible]

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## **FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVRVFPFVWGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDEQ  
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAG  
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT  
CCGTACCTCTCCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGCCAGGTGTTT  
GGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTGTCT  
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTCTTTCAGGGGCCAGTTCTCTAGCGTGG  
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCACAGTCTTACTACCAGAAGGCCA  
TCTGGGAGCTACAGGTGTCTGAGTCTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTT  
GATAGAGACATCCAGCTACTCTGTCTGAGTCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG  
GAAAGGTCACAAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA  
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAATCCAGGCGGAAGTGGAC  
TGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCCGGAACACGCAGTGAGGTGAC  
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAAGAGTGTGGTGGCT  
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCTGACTATGAGTG  
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT  
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAAGTCCC  
ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
AATCCCAGAGACAAGCAACAGTGAGTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
GTGAAATGT**AGG**ATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
ACATGGGAGTCAGGTGTCTGAGTCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATT  
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACC  
TCAGGAATTCCTATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
AAAAAA

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## **FIGURE 92**

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPQGQDLSTDSRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRTPTPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSSQATT PFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255



**FIGURE 93**

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG  
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG  
 GACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTAGGGCCGACGGC  
 TCCACGCCCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
 ACCACCTTTTCAGGCGCCGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC  
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCCG  
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCC  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
 TTGCGCTCCTCAGAGTGTATGTAAGTCTGTTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
 TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATAACCGTGCAACAGGTAAGCAACAGAGGGTGGAACTGAAGTTTATT  
 TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT  
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAG  
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGA  
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGTTTAGAAATGTTCTT  
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA  
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA  
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAG  
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
 ATAATGTACTGTTATCTAAGCATTTGCCTTGCTACTGCACTGAAAGTAATTTCTTTGACCT  
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAAT  
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTTCTTCTCAAG  
 GTTGTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGGTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAG  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTTAAAAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA  
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
 GCACTCCAGCCTGGTGAGAGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRSLSLGGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPPLWATAGPSSTTFQAPLGPSPTTTPPAAERTS  
TTSQAPTRPAPTTTLSTTTGPAPTTVPATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTC  
CACAGCA

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## **FIGURE 96**

MGGLLLAAFLALVSVPRQAVWLGRDLPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCC  
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
GGCTGGATTTACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAAATGGAATTATAA  
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC  
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
AGAGCAAAGCCACATCAGGAGTGA CT CAGGGGGTGGT CGGGGGAGCTGGAGCCACAGCCCTG  
GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGT CAGGGGTTCAGCCT  
CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
ACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCAGAGCCCCCTCCAGGCAAGGGA  
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

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## **FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSSYP SHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHL LGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPQNLTMTV FQGDG  
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDTGIEDANAVRG SASQGPLTEPWAEDSPPDQPPPASARSSVGE GELQYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCTGGAGAGATGAAGACCCTGTTCCCTG  
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAATAAAGTCCT  
TTTCCCCCAA

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## **FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL

EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH

MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:**

**Signal peptide:**

amino acids 1-17



**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCCACCCTGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA  
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTTCTGTTCACTCTGTTAAT  
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW  
AVRPLTLSSRCVTAGTSCGISGSGTSSPQLRLPHTLRCANITIIHQKCNAYPGNITDTM  
VCASVQEGGKDSCQGDSSGGLVCNQSLOGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCCTTGGTGTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTAAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCTATGAGAAGATATTTTGA  
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDIFKKNHDHGDGFISPKEYNVYQHDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

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## **FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

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**FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG  
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGGCAC  
CAGCCTGCGCTGCGGGGTGTCCTTATTGACCACAGGTGGGTCTCTACAGCGGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCTTGCCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC  
ATCACCACACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC  
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACCT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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## **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVPCGQDGIPGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17



**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**  
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTTCATTGAGGGTTTGTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC  
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTTGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGACGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAAGTGAGGCCTG  
GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAA

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**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

**FIGURE 111A**

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCACACCA**ATGG**CCCCCGGGTGGGCAGGGGTCGGCGCCGCCGTGCGCGCC  
CGCCTGGCGCTGGCCTTGCGCTGGCGAGCGTCTTGAGTGGGCCTCCAGCCGTGCGCTGCC  
CACCAAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTT  
CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAAAACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT  
GAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTGGAGATCCTTACCCTCAACAACAACATCAGTCGCATCCTGGTCACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCAACTCT  
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCCCAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC  
CTGACAGTGCAACAATAACATCGTGGACTGTCGAGGAAGGGCTTGATGGAGTACCCGATGT  
ACTTGCCGGAGGGCATCGTCGAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA  
AGATCACCAGGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT  
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCCGCGCCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTCCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG  
TGTGAGGGCACGATTGTGGAAGTGTCTCAACCCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC  
TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT  
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA  
GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGTCTCCCT  
GTCCACCATAAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCCTAGGTGCCAGAAGCCATTTTTCTC  
AAGGAGATTCCTATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTCTGAAGG  
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGAGTCTTCGCTGTGTCGGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGCCATCGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
GCATGGAGGACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCACTGCTCCTGCCCTC  
TGGGCTTTGAGGGGACGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
AACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC  
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTGAGCATG  
AGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG  
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGCCCAGTG  
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCCTTCTGTG  
AACACCCCCCAGCCATGGTCCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC  
GGGGCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG  
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG  
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT  
GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA  
ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG  
GACAAAGGAACTCCAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
CCCCCTCTACCTTGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGGCACGG  
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTACCAGGCTGCAAGTCTGCACCGT  
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCCAG  
GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG  
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCCTGTGCCAGCCCGGCTTTAGCGGC  
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT  
GTGGGCCCCAGTGCTGCCAGCCCACCCGAGCAAGCGGCGGAATACGTCTTCCAGTGCACG  
GACGGCTCCTCGTTTGTAGAAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC  
CTAAGCCCCCTGCCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
AGAGAATATTAAGTATATTGTAAAATAAACAAAAATAGAACTTAAAAAAAAAAAAAAAAAA  
AAAAAA

**FIGURE 112**

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL  
PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL  
TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
EIRLEQNSIKAIPAGAFQYKCLKRIDISKQISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
AQNPFVCDCHLKWLDYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIRSRFS  
SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
SNDTFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRR  
IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR  
ALPRGMPKDVTELYLEGHNLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL  
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL  
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFOCKGPVDINIVAKCNACLSSPCKNNGT  
CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR  
CEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL  
DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV  
LLQTSPCDQYECQNGAQCIVVQQEPTCRCPGFGAGPRCEKLI TVNFVGKDSYVELASAKVRP  
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS  
VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSV VCECRPGWTGPLC  
DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHGQCHISD  
QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQ  
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

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## **FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGAAAAAAGGCTGTGAGGTTTCTCTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA  
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

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## **FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDAAICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

**FIGURE 115**

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCC  
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACCTCCCAGATCTGCTTCTCAC  
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG  
CTTTGACTCAGTTGTTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC  
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT  
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA  
ATAGAAAAGTTCATCCGTGAACCTTCTTAAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
AGTGAAGGAAAAATTTTCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC  
TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA  
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
TCATTCCATGTTTACGAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA  
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT  
CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTGTGTTGCTGTCTTGCCTGGATC  
CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTTGCACACTGAGATATAA  
TAAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRRLARRRKKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTT  
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT  
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCC  
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTCAC  
TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTTCATTGACTC  
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA  
GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC  
AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTTCGAACTGCCA  
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT  
CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT  
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
ATTAAAATTTTATACATTTAAAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA  
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
TTAA

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## **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTS EEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETIVLYALGVVL  
QDPNTWPSPHKFD PDRFDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCTGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTACCCGTCTTTGGGCTGAAA  
AAGAAACCCCTTCTGAATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTTCCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTTAGGGGACA  
ATTAAAAAAAAAAAAA

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## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

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## **FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACTATGTTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCCGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC TTCAGGGGTGC  
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAAC TATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTTGAGGCC  
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

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## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT  
GACTCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
CGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
CGAACCACAGCCCCCACCCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC  
GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCTACTACCCATC  
TGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCAATGGGAGGAAGCTAAGCCCTTGATT  
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCGTGTGCTGAGCATG  
GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
CAGCCAGGCCACCCCTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCTCCACACTAAGGCC  
ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGTCTCTTGGGAG  
CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCTCC  
CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGA  
GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT  
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAGCTT  
GCCCCGGGGCA



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## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY  
YPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA  
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG  
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
 TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTTCGACCTAGCCGCTAG  
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
 GGCTGCGGCTGCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
 GCCGTGCTGCTGGTCTCAGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
 CATCGTGTGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACC CGGCCACGGACTCCAAGG  
 GCTCCTCTTCCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
 CGATCAGATCCTGGTGAATGTGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
 GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG  
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGTCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG  
 TTCCCCCTAAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAGATCATTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
 TGTGTCTGTTTTAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
 ACAGTCAAAGCTGTCTGCAAGACTTATTCTGAATTTTCAATTTCTGGGATTACTGAATTAGT  
 TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGGTTCTTGTA  
 AAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
 TGGCTTGCCCAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAAA  
 GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTTATTGC  
 TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAACCTAAGGTTTTTTTTTTTT  
 TCCGTAGACATGACCACTTTATTAAGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
 TTTTCAAGGCTTCTGTTGATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
 CTTGTCTTTTGTATAGGTATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA  
 TTAATATATGTTAAAAAAA

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## **FIGURE 126**

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSPATDSKGSSSSPLGI  
SVRAANSKVAFAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFAVPRKGIYSFSF  
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTTGTATTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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## **FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658  
><subunit 1 of 1, 257 aa, 1 stop  
><MW: 28472, pI: 9.33, NX(S/T): 0  
MTAAVFFGCAFI AFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF  
GIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRSCLKCLLCQDKN  
FLLYNQRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTTCGCTCTGGGCTTGCCCTTC  
 TTGGTGTCTCTTGGTGGCCTCGGTGCGAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGC  
 CGAGTTTGGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGA  
 CCCGCAACAGGACAGAGGGCGTGCCTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCGTGTGTTT  
 GTGGTCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTA  
 CCTTACCAAAAAGTGAACGAACCCCTGTGTACGCCCCCACCAGAATGAGTCGGAGATTAGTTCCTTCTACG  
 TGGATGTGTCCACCCCTGTCAACAGTCAACACCACATACCAGCTCCGGGTACGCCGCATGGACGATTTTGTGCTC  
 AGGACTGGGGAGCAGTTACGCTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCTGAAGG  
 CGTGGACTCGGTAAATTGTCAAGGTGACCTCCAACAAGGCCCTTCCCTGCTCAGTCATCTCCATTAGGATGTGC  
 TGTGCTCTGTCTATGACCTGGACAACAACGTAGCCTTTCATCGGCATGTACCAGACATGACCAAGGCGGCC  
 ATCACCGTACAGCGCAAGAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGC  
 CTGCGGGGGCTCCCTGCCCTTCTACCCCTTTCGAGAAAGTGAACCGGTGATCAAGGGCACCGCCAGAAAACCC  
 TGTGACTGCTGGTGTCTCAAGCAGTCACGTCTGAGGCATACGTAGTGGGATGCTCTTTTGCCTGGGTATATTT  
 CTCTCTTTTACCTGCTGACCTCTCTGCGCTCTCTGGGAGAACTGGAGGCAAGAAGAAGACCTGCTGGT  
 GGCCATTGACCGAGCCTGCCAGAAAGCGGTACCCCTCGAGTCTGCGCTGATTCTTTTCTGCGAGTTCCCTT  
 ATGAGGGTTACAACATATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTGGACGCGCTGGCACT  
 GGGGACCTCTCTTACGGTTACAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAG  
 CTCTGTGGAGGAGGATGACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCAATCGCACCAAGCAAT  
 ACCTCTATGTGGCTGACCTGGCAGGAAAGGACAAGCGTGTCTGCGGAAAAGTACCAGATCTACTTCTGGAAC  
 ATTGCCACCATTGCTGTCTTCTATGCCCTTCTGTGGTGCAGCTGGTGTATCACCTACCAGACGGTGGTGAATGT  
 CACAGGGAATCAGGACATCTGCTACTACAACCTTCTGCGGCCACCCACTGGGCAATCTCAGCGCCTTCAACA  
 ACATCTCTCAGCAACCTGGGTACATCTGCTGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAAC  
 CACAACCGGGCCCTGCTGCGCAATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTA  
 CGCCATGGGCACAGCCCTGATGATGGAGGGCTGCTCAGTGTCTGCTATCATGTGTGCTATCATGCTTCAACAT  
 TCCAGTTTGACACATCGTTTACGTACATGATCGCCGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCG  
 GACATCAACGCCAGCGCTACAGTGCCTACGCGCTGCTGGCCATTGTCTCTTCTCTGTGCTGGGCGTGGT  
 CTTTGGCAAAGGGAACACGGCGTTCTGGATCGTCTTCTCCATCATTCACATCATCGCCACCCCTGCTCCTCAGCA  
 CGCAGCTCTATTACATGGGCCGCTGGAACCTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACA  
 GACTGCATCCGGCAGTGCAGCGGGCCGCTCTACGTGGACCGCATGGTGTGCTGGTCAATGGGCAACGTCAAC  
 CTGGTCTGCTGGCTGCTATGGGCTTATCATGCGCCCCAATGATTTCCGTTTCTACTTGTGGCCATTGGCATCT  
 GCAACCTGTCTCTTTTACTTTCGCTTCTACATCATCATGAAGCTCCGGAGTGGGGAGAGATCAAGCTCATCCCC  
 CTGCTCTGCATCGTTTGCACCTCCGTGGTCTGGGCTTTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACCTG  
 GCAGAAAACCCCTGCAGAGTCGAGGGAGCACAACCGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACA  
 TCTGGCACTTCTCTCTCCATCGCCATGTTTCGGGTCTTCTCTGGTGTGCTGACACTGGATGACGACCTGGAT  
 ACTGTGACGCGGGACAAGATCTATGTCTTCTAGCAGGAGCTGGGCCCTTCGCTTCACTCAAGGGGGCCCTGAGC  
 TCCTTTGTGTATAGACCGGTCACTCTGTGCTGTGTGGGGATGAGTCCAGCACCGCTGCCAGCACTGGATG  
 GCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCTGGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCC  
 CTCTGCCGAGGAGCAGGCCTGCTCCCTGGAACCCCAAGATGTTGGCCAAATTGCTGCTTTCTTCTCAGTGTG  
 GGGCCTTCCATGGGCCCTGTCTTTGGCTCTCCATTGTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCCCT  
 CCCCATTTCATGCCCTGCATTTTGGCCGCTCTCTCTCCCAACATGCCCCAGCCTGGGACCTAAGGCCTCTTTT  
 CTTCCCACTCTCCACTCCAGGGCCTAGTCTGGGCTGAATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTT  
 GGGCTGTCTCTGGCTGCCATCACTGCCATTCCAGTCAGCCAGGATGGATGGGGGTATGAGATTTTGGGGGTTG  
 GCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGGCTGGGGCAGTGCCTATTCTCTTCCCTCTGAC  
 CTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATTGAGAACCCTCTCTGATTCAAGAGGCTGAA  
 TTCAGAGGTCACTCTTTCATCCCATCAGCTCCAGACTGATGCCAGCACAGGACTGGAGGGAGAAGCGCTCA  
 CCCCTTCCCTTCTTCTTCTTCCAGGCCCTTAGTCTTGCCTAACCCAGCTGGTGGCCTTTCAGTGCCATTGACAC  
 TGCCCAAGAATGTCCAGGGGCAAGGAGGATGATACAGAGTTTCCAGCCGTTCTGCTCTCCACAGCTGTGGGCAC  
 CCCAGTGCCTACCTTAGAAGGGGCTTCCAGGAAGGATGTGCTGTTTCCCTCTACGTGCCAGTCTAGCCTCG  
 CTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCCAGGCAAGTTCTGTGTTAGTGCACACACA  
 TACCTATGAAACCTTGGAGTTTACAAGAATTGCCCCAGCTCTGGGCACCCCTGGCCACCCCTGGTCTTGGATCC  
 CCTTCTGCTCCACCTGGTCCACCCAGATGTGAGGATGGGGGAGCTCAGCGGGGGCTCTGCTTTGGGGATGGG  
 AATGTGTTTTTCTCCCAAACTGTTTTTATAGCTCTGCTTGAAGGGCTGGAGATGAGGTGGTCTGGATCTTT  
 TCTCAGAGCTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATTTGCATTCAATAAACACCCAGAC  
 TCAAAAAAAAAAAAAA

## FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT  
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE  
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI  
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV  
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTL SVLV SQAVTSEAYVSGMLFCLGIFLSFYLL  
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL  
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL  
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN  
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGFLFYAMGTALM  
MEGLLSACYHVCPTYTNFQFDTSEMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS  
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG  
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI  
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA  
MFGSFLVLLTLDDDLDTVQRDKIYVF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

#### **Leucine zipper pattern.**

amino acids 497-518

#### **N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG  
 ACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACCTATGGTGGAAATTTCCCTTTTATACC  
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA  
 GGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAG  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAGGCCTGGCATCCC  
 CTTCTCTTCTTGGAGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCTTTGAAGTGAATGCAGAGGGAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC  
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCAGTACAGATATCAATGATACGCCCCCTGAGTTCATCTCCAGAT  
 TGGGCCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA  
 TACAGCCCTGACTCTTGCCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGAACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTT  
 CCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTGCTGCAAC  
 GTGGAGGGGCAGTGATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGC  
 AGTGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTCACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCCTGAAGGCG  
 ACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGCTCAAATGTCAGGGTGTTTGCCCAATAATAAGCCCCA  
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG



**FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQA EYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSI IESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLMVDENDNVPICPPRDPVTISIPELSPPGTEVTRLSAEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLP LRAQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLT AIDADLEPAFRLMDFAIERGDTE  
GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPI SRTLRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHII PVVSHNAQMWQLLVRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCCTGTGGATGTCTTGGTCCCATCTGTGAGTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC  
 CTGGCGAGGAGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCGTGAGGCGGCCGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTCCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTGCAGGAAAG  
 GGAGCCAGCGACAACCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCACTGA  
 GTACCAAGTGGGTCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC  
 TTCTCCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGTCCTGGCGGTGTCCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTGGTCTCTG  
 CTGTTTTTGATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC  
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAGAACATC  
 TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT  
 TCGCAGTCTTCTGGAAAATATTTTCTTTTGGAGCAGCAAATCTTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGTC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCA  
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCCCCCTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTGTATTTCAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTGCAGGATGGTGAATTTATCCCCATCTGTCTAATGGGCTTACCTCCT  
 CTTTGCCTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATCCCATTTGTGTCTGTGGTGTATCCTGTGTT  
 TCCTTGTCTGGTTTTGT  
 TCTGTCTATTTTGTATCCTGGACCACAAGTTTCTAAGTAGAGCAAGAATTCATCAACCAGCT  
 GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGTGT  
 TTGTTTTTTTTGCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAETWLGLKTIMEHVRDONLY

**Signal peptide:**

amino acids 1-16

[illegible]

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## **FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

[illegible]

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNSDSSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVSIIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAATATGCATCTTGACAGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTTGTGAATAAACTTGATACACCA



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## **FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNQASKEANQLLNHNHQS GSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

CTCGGGTCCCCAGGGGCTGCGCCGGGCCGGCCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGG  
 CCCCCGGGGGGGGCGATAGCCGTGCGCTGACCCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCCGGGGCGACT  
 CGGGGGCGGACCGCGGGGCGGAGCTGCCCGCCCGTGAAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGACACC  
 TCGCTCTCTGCTCTCGAATGCTGCGCACCGCGATGGGCCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCT  
 GCGCCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCAGCCGCCGCTCCGACCTGGGCGC  
 TCAGCCCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGGAAGCTGAACACATCTCC  
 AACTACACAGCCCTTCTGCTGAGCAGGATGGCAGGACCTGTACTGCTGGGTCTCGAGAGGCCCTCTTGCAT  
 CAGTAGCAACCTCAGCTTCTCTGCCAGCGGGAGTACAGGAGCTGCTTTGGGGTGCAGAGCCAGAGAAGAAAC  
 AGCAGTGCAGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCTCGCCGCTCAG  
 GGCAGTCACTGTTCACTGCTGGGCAGCAGCCTTACGCCCATGTGTACTCATCAACATGGAGAACTTCA  
 CTTGGCAAGGACGAGAAGGGGAATCTCTCTGGAAGATGCAAGAGGCGTTGTCTCTCGAACCGAATTTCA  
 AGTCCACTGCGCTGGTGGTTGATGGCGAGCTCTACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCC  
 ATCTCGCGAGGCCAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAGAGCCAGCTTTTGT  
 GGCTCAGCCTACATCTCTGAGAGCCTGGGCAAGCTTGAAGGCGATGTACAGAAGATCTACTTTTCTTCAGCG  
 AGACTGGCCAGGAATTTGAGTTCTTTGAAACACCATTTGTGTCCCGCATTTGCCCGCATCTGCAAGGGCGATGAG  
 GGTGGAGAGCGGGTGCTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCCGACGA  
 TGGCTTCCCTTCAACGTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGCACACCTTT  
 TCTATGGGGTCTTCACTTCCAGTGGCACAGGGGAATCAGAAGCTCTGCCGTCTGTGCTTCAATGAAG  
 GATGTGCAGAGACTTTCAGCGGCTCTACAGAGAGGTGAACCGTGAGACACAGCAGTGTGTACACCGTGACCCA  
 CCGGCTGCCACACCCCGGCTGGAGCGTGTCATACCAACAGTGGCCGGGAAAGGAAGATCAACTCATCCTGCG  
 AGCTCCCCAGCCGCGTGTAACCTTCTCAAGGACCACTTCTGTAGGACGGGCGAGTTCGAAGCCGATGCTG  
 TCTGTGCAGCCCGAGGCTCGCTACCGAGCGTGGCTTACACCGGTCTTGGCTGCACACACCTACAGATGT  
 CCTTCTCTGGGCATGGTGACGGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGG  
 AGCTGCAGATCTTCTCATCGGCAGCCCCGTGAGAATCTGTCTCTGGACACCCAGGGGGCTGCTGTATGCG  
 GCCTCACACTCGGGCTAGTCCAGGTGCCATGGCCAACTGACAGCTGTACCCGAGCTGTGGGACTGCCCTCT  
 CGCCCGGGACCCCTACTGTGCTTGGAGCGGCTCAGCTGCAAGCAGCTGAGCTCTTACCAGCTCAGCTGGCCA  
 CCAGGCGGTGGATCCAGGACATCGAGGGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCCG  
 TCTTTGTACCAACAGGGGAGAACGCACTGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTG  
 CCCGCTCCTCTCAACCTGGCGAGCCGCACTGTGGCTACGCAACGGGGCCCCCGTCAATGCCCTCGCCTCTGCC  
 ACGTGCTACCCACTGGGACCTGCTGCTGGTGAGCACCACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAG  
 GAGGGCTTCCAGCAGCTGGTAGCCAGTACTGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGA  
 GGGTGGCAGTGATCCCGCTATTACAGACACTCGCTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTG  
 CAGACAGGTCTACTGGAAGGAGTTCTGGTGTGTGACAGCTCTTTGTGTGGCGGTGCTGCTCCCAAGTTTAA  
 TTCTGTCTCAACGGCACCAGAACAGCATGAAAGTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGCACCCCAA  
 GACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGCCACTCAACGGCTAGGGCCCCCTAGCACCCCGCTCGATC  
 ACCGAGGGTACCAGTCCCTGTGCAGACGCCCCCCGGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACT  
 AGCATCCAAGACAGCTTCTGTGGAGGTATCCCCAGTGTGCCCCGGCCCGGCTCGCCTTGGCTCGGAGATCCG  
 TGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGCTGCCCTGGCTTACGGGGCTGTGAATGCTCGGAGAGGG  
 TCAACTGGACCTCCCCTCGCTCTGCTCTTCTGGAACACGACCGTGGTGGCCGCCCTTGGGAGCCCTTGGAGC  
 CAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCTTACCACCCAGACACCCAAACAGCCGCTGCCCCAGA  
 GGTCTGGCCAAATATGGGGGCTGCCTAGGTTGGTGGAAACAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAA  
 AAAAAAATTTCAAATGTGAACTAGAATGAGAGGGAAGAGATAGCATGGCATGCAGCACACCGCTGCTCCA  
 GTTCATGGCCTCCAGGGGTGCTGGGATGCATCAAAGTGTTGTCTGAGACAGAGTTGGAACCCCTCAACAA  
 TGTGCCCTCTTCACTTCCACATTATCCGCTGCCACCGCTGCCCTGTCTACTGCAGATTGAGGACAGCTTG  
 GGCTGCGTGCGTTCTGCTCTGCGAGTCAGCCAGGATGTAGTTGTTGCTGCCGTGCTCCACACCTCAGGGAC  
 CAGAGGGCTAGGTTGGCACTGCGGCCCTACCAAGTCTGGGCTCGGACCCAACTCCTGGACCTTTCCAGCCTG  
 TATCAGGCTGTGGCCACAGGAGGACGCGCAGCTCAGGAGAGATTCTGACAAATGTACGCTTTCCCTCA  
 GAATTCAGGAAGAGACTGTGCTGCTGCTTCTCCGTTGTTGCTGGAACCCGCTGTGCCCTTCCCACATAT  
 CCACCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACCTTGGTCTCTCCCCAGTCCCCAGTTC  
 ACCCTCATCCCTCACCTTCTCCACTCTAAGGATATCAACACTGCCAGCACAGGGGCCCTGAATTTATGTG  
 GTTTTTATACATTTTTTAATAAGATGCACTTTATGTCATTTTTTAATAAAGTCTGAAGAATTACTGTTAAAAA  
 AAAAAA

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCP  
FDPNFKSTALVVDGELYTGTVSSFQGNDDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGGDDDKIYFFFSSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP  
QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPPVLPETRPPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACC  
AGCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCGCCGCTCGTGCCTG  
CGTGCCGCGCCCGCGTCCCCGCGCGGAGCGGGAGGAGCCCGCCACCTCGCGCCGAGCCGCGCTAGCGCG  
CGCCGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGCGGGGGCGGGTGTGCGGAACAAAGCCGCGCGC  
GGGGCTGCGGGCGGCTCGGGGCGCGCATGGGCGCGGCGGGCCCGCGGCGGCGCGGCGCTGCCGCGGGCGGG  
CCTCGCGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGCGAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGC  
GGCGGCGGCGGCGGCGGCGGCGGCGGCGGGCGGAGCGGCGCGGGCATGGCCGCGCGCGGCGGCGCGCCTGGCTC  
AGCGTGCTGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCGAGCTGAA  
GCGAGCGGGGCCACGGCGCCGCGCCAGCCCCGAGGGCTGCCGCTCCGGGCGAGCGGCGGCTTCCAGGCCGCG  
GGGCGCGGCGCGATGCGCGCGGGGCGCAGCTCTGGCCGCGCGGCTCGGACCCAGATGGCGGCGCGCGCAGAG  
AACTTCTCTTTCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATG  
GTCCAAAGACAATTTCTGGGAAAGTTCAAGTTCTTCTCAAGTGAGGTTCTGACACATCTGTACCAATTCAGTAG  
TGCCACTACGGGGTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCCTTCATGATGCTCAAGTACATGCACGAC  
CACTACTTGGACAAGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAA  
CTTCTGAGGAGTTTGAACAGCAGCGAGCCCTCTTCTTGGGCAGACAGGCCTGGGCACACGGAAGAAATGG  
GAAACTGGCCCTGGAGCCTGGTGAGAACTTCTGCATGGGGGGGCGCTGGCGTGATCATGAGCCGGAGGTGCTT  
CGGAGAATGGTGCCGCACATTGGCAAGTGTCTCCGGGAGATGTACACCCCATGAGGACGTGGAGGTGGGAAG  
GTGTGTCCGGAGGTTTGCAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTTTATGAGAATTACG  
AGCAGAACAAAAGGGGTACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATACATTACCCCAAC  
AAAAACCCACCCCTACAGGTACAGCTCCACAGCTACATGTGAGCCGCAAGATATCCGAGCTCCGCCATCGCAC  
AATACAGCTGCACCGCGAAATTTGTCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGC  
TGGGAATCCCTCCCTCCTTCATGAGGTTTTCAGCCCCGCGCAGGAGAGATTTCTGGAATGGGAGTTTCTGACT  
GGAAATACTTGTATTCGGCAGTTGACGGCCAGCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTT  
GGACGACATTGTCTATGCAGGTCTATGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCA  
AAGAGATCCAGTACGGCTACCGCGGGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTG  
TACAAAAGCACAAGGGAAGAAATGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTTCAGCAA  
AATCCAGTTTGTGGAGCATGAGGAGCTGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCT  
TGTCCTTTCTCTCAAACCTCCCTGAAGAAGCTCGTCCCCTTTCAGCTCCCTGGGTGGAAGAGTGAGCACAAGAA  
CCCAAGATAAAAAGATAAACATACTGATTCCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAAA  
CTTTGAGAAGACGTGTCTTATCCCAATCAGAACGTCAGCTCGTGTTCTGCTTTTCAATTTCTGACTCCAACC  
CTGACAAGGCCCAAACAAGTTGAACGTGATGAGAGATTACCGCATTAAGTACCTAAAGCCGACATGCAGATTTTG  
CCTGTGTCTGGAGAGTTTTCAGAGCCCTGGCCCTGGAAGTAGGATCCTCCAGTTTAAACATGAATCTTTGCT  
CTTCTTCTGCGACGTCGACCTCGTGTTTACTACAGAATTCCTTCAGCGATGTGAGCAATACAGTTCTGGGCC  
AACAAATATATTTTCCAATCTTCAGCCAGTATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCCGTGAC  
AACCATTTTGCCTTTACTCAGAAAACCTGGCTTCTGGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGG  
AGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCATCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACA  
AGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCCAGGAAGTAGGAGTAGTCCAGTCCACCATTCTGTCTTT  
TGTGATCCCAATCTTGACCCCAAACAGTACAAAATGTGCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCA  
GCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAAGTTACAGTAAAAGCAGCAATAATATGGCTCAGTGA  
GGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTTTAATTATCTAATTTATTTTTCAAAAATTTTTTGTA  
TGACTAGTTTTTGAAGTCCGTATACAAGGATATATTTTACAAGTGTTTTCTTACATAGGACTCCTTTAAGATT  
GAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGACCTTTGAACACATCTTCTGCTGAACATTATGTAGCAGAC  
TGCTTAACCTTTGACTTGAAATGTACCTGATGAACAAAACCTTTTAAAAAAATGTTTTCTTTTGAGACCCCTTG  
CTCCAGTCTTATGGCAGAAAACGTGAACATTCCTGCAAGTATTATTGTAAACAAAACACTGTAACTCTGGTAAA  
TGTTCTGTGTGATTGTTTAAACATTCCACAGATTCACCTTTTGTGTTTTGTTTTTTTATCAATTTGTTTTTA  
AAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATAGCTGTTTCATCATTGTCTTCAGGAGAGCT  
TTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGCCACGTAGGTTTTTTGTTGTTTTGTTTT  
GTTCTTTTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATGCAGTGGCGCAATCTTGGCTCACTTTAA  
CCTCCAGTTCCCTGGTTCAAGCAATTCCTGCTTTGCTTCCGAGTAGCTGAGGATACAGGCACACACCAC  
ACGCCCAGNTAGTTTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCATGCAAGCCAGCTGGCCACGTAGGTT  
TTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCGTGAGTTTCAATTCGGCCTAAATAG  
ACCTGGCATTAAATTTCAAGAAGGATTGGCATTCTCTTCTTGACCTTCTCTTTAAAGGTTAAATATTAA  
TGTTTAGAATGACAAAGATGAATATTACATAAATATCATGTATGACAGACTGAAACATACACACATACCCCT  
AATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCCCTTCATCCTGTCTGTGTTATGTGGGTGGAGATGGT  
TTTCATTTCTTACTTGTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAATTTATTTAATATCTGTTGTT  
CAGAGCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTTATGTGTATCGGAGTGTGTTAGTCTGTTT  
TATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTTCCCCTCC

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## **FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGG  
GGACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTG  
TTTTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAA  
TAGCCTGATGCTCATTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTGTCT  
CATTATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAAA

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## **FIGURE 144**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGLVVRVGGFVDSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC  
TAACTCTCCAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAAGAAAAACACACGGAAAGTACCCC  
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAAATGAAGAGCCAGAGCCAGAGCCGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
CAGGTGAACTGCGATAGAAAAACCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT  
GATGACATTTTGAAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCA  
GTAGGACGAACAAGTAATAAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC  
TAGATCTAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
AAAGTTTATTAACAATAATATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA  
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTATGTGTTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAAATTTTGGTTCAGGAAAAA

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## **FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAEOPYIENEPEPEPEPAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPPEEFGKHPESWNNDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSL  
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19



**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
ACCTCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTTCATAGTGTGAGATCAACCCACA  
GGAATATCCATGGCCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
CCTGCTCCCTCTTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGC GGTTCTTCAGGAATCAG  
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
GTATCGAGGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGGCGTGTCTCTCTAAGGC  
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTCAT  
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC  
CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
GCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA  
GGCGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACAG  
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTCGTTCATCTGATAAGGAA  
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACAATGTG  
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTCC  
ATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
CTGCTGACATGTGAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA  
GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTGCGGATGAGACAGAGAAGACCCTG  
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC  
CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAGC  
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCAGATGAGGGGGGAT  
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
CATTAGGTTTGTGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTGCTCAGGTCACAGGTGAAGATTAAAGAGA  
CAACGAATGTGAATCATGCTTGCAGGTTTGGGGGCACAGTGTGCTAATGATGTGTTTTTA  
TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA  
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
GAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAACCAGGCAAAG  
AAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAA  
TTCTAAATAAAATTTTAAACAAATTAACCTAAACAATATATTTAAAGATGATATATACTACT  
CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAATT  
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

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## **FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIVQENAGSILCSIHLEQSQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC  
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA  
 TTAATATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAATTGTTCAACTGTTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
 GATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
 GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGTTTGTGACAGGATTTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGAATCTGGAGGACCACTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAG  
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGACTGGATTACTTCAAAAACCTGGTATCTA  
 AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGCAATTTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCAATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
 ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

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## **FIGURE 150**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD  
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR  
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL  
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG  
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYTNAVHRVCLPDASYEFQPGDV  
MFVTGFGALKNDGYSQNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD  
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
CAGATGAGACTGAGACGGCGTGCGCCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCGGCGGCCCTGCCTGTGCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCTCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCGTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
CCTGCCTTCGGGCCTTGACAGCCGCCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC  
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGCGATCGCTGGGGCTGCCC GCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTCTGA  
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA  
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPLGLSSPAQPPDPMPGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA  
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRV PQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTL VHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGG  
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACAAATGGCCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGTCATGGTACT  
 TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACTTATGGTTCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTTTTTCAGAGAGAGTTTAAAGT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAAACTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC  
 CTTGAAGAATGACAACTCTCAGCACCTGTCTGTCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTATTAAAAAGAAATGTACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT  
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAACTTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA  
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAAATTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 . ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTGAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
 GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG  
 AAGACTCTTTTTGACACTAAACACTTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA  
 GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAAATAGTGTTCTTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA  
 ATATACTGTGGCAAATTACACAGATTATTAATTTTTTACAAGAGTATAGTATATTTATTT  
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTTTCTCAGAATATGGAA  
 AGAAAATTAAATGTGTCAATAAATATTTTCTAGAGAGTAA

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## **FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ  
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF  
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG  
TGATTCTGGATAAATACTACTTCCCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG  
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG  
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC  
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT  
GTGGTGGGTGGGGAGGAGGCTCTGTGGATTCTTGCCCTTGGCAGGTCAGCATCCAGTACGA  
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCCAT  
GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC  
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA  
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC  
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
TGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC  
CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
GGGCCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTG  
CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC  
CTCTGCCCACAGCCTCAGCATTCTTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC  
TCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
GGAACTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA  
CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
CTGGCAAAAAAAAAA

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## **FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF  
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF  
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL  
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV  
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNNDIALMKLQFPLTFSGTVRPICLPFFD  
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE  
GGVDTCQGDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCA  
 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGG  
 CCTTTTCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGC  
 CCAGGGTCAGATACTATGCGAGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTT  
 GACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATAT  
 CCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTG  
 CCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTTCTTACAATGTACCCCAT  
 CTCTACACCTGCGGCACCTTCGCTTCAGCCCTGCTGTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCC  
 CATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCCTTGACCCCGCTCACAAGCATACGGCTGTCT  
 TGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTG  
 GGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCGCTGGCTGCATCATGACGCCTCCTTGTGGCAGCCAT  
 CCCTTCGACCCAGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACA  
 CATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC  
 CTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCTATCCGCCACGCGGTCTGTCTCC  
 CGCCGATTCTCCACAGCTCCCAACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACAGGAGCT  
 CTGCGGTTTGTGCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA  
 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGCCAGGCAGTTGCTCAGTGGGCCCCCTCTC  
 TGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTGA  
 AATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCCAGGGCCTTGATGGGACAGCCATCTTGTCTAG  
 TACCTGGGAACCACCACAGGGTGCCTCCACAAGGCTGTGTGAAGTGGGGACAGCAGTGTCTATCTGGTGAAGA  
 GATTGAGCTGTTCCCTGACCTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTGTAG  
 GCTTCTCAGGAGGTGTCTGGAGGGTGGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTT  
 GCCCGGACCCCCACTGTGCCTGGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTC  
 CTGAAGCAGGACATGGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGC  
 CTCAGAGCCGCCCAATCATTAAAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCAC  
 CTGTGACGCTTGGCCTCTTATTATTGGAGTCATGGCCACAGCAGTCCAGAAAGCCTTCCACTGTCTACAA  
 TGGCTCCCTCTGTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTTT  
 CATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATC  
 CCCCGGGAGCATGTGAAGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTCTACTG  
 GCCCACTTTGTCACTGTCACTGTCTCTTTCGCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  
 CATTGAGAGCACTCCGGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTA  
 AGCAGAGAGCAACACCTCCAGTCTCCAAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTG  
 CCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGG  
 GCGCCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCGAGAGGAGCTTCTG  
 CTACTCTGCATCACTGATGACACTCAGCAGGGTGTGACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTAC  
 CAAGCACATGAGCTCTCTAACAGGGTGGGGGTACCCCCAGACCTGCTCTACACTGATATTGAAGAACCCTGGA  
 GAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGC  
 CTGTCCCAGGACCTATGGTAATGAACACCAACATCTAACAATCATATGCTAACATGCCACTCCTGGAACT  
 CCACTCTGAAGCTGCCGCTTGGACACCAACACTCCCTTCTCCAGGGTCATGCAGGGATCTGCTCCCTCCTGC  
 TTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCA  
 GTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGTAATCTGAGCCTTCTTCACTCCTTTACC  
 CTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTCCCTTTGTTTGGGATTGAGAAAAGCTGTGTGAGAGACTG  
 TTTATTTTTTATTAAAAATATAAGGCTTAAAAAA

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## **FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ  
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA  
VLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE  
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN  
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP  
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
HFVTVTVLFLVLVSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
SASDVDADNNCLGTEVA

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704



## FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGGCTTCCGTAGAAG  
 TGAGC**AT**GGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA  
 GTTGAACTTTTGGACTACTGTCTTTCTCTGATTGCTGAGAAGCTTGGAAGCCATTTGTGGC  
 CATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT  
 CAGTATTCGGTTCTTGGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCATTAACCTCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC  
 CAAGTTTGGGACTCTGGTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA  
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCAAGTGTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTTGTGA  
 CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG  
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTT  
 AAAGAAGCTCAAGGCAGAGACATTTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
 TGTCTTTTCAAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACAT**TA**AGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC  
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
 TAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT  
 CTTGTCTCCTTTGTTTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA  
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTAGTTTTCTGTTT  
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGC  
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAAAATAAAAGTTTACA  
 GCGTTATCTCTCCCAACCTCACTAA

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## **FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIPLSYVPV  
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF  
INSDFAFDFAFARLLPNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPPQGVWKCQCQSHWPKDVHAAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ  
NSIMEAIQHGVPVMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPWHEQYLFDFVFLGLT  
LGTLLWLCGKLLGMAVWVLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT  
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAC TGCACTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGAAACAGAAGAGGGGCAGA  
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC  
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCC  
 GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
 GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTGTTGAACGAGGGCGGTGGCTTTGACCGGGC  
 CTCTGGCTCCTTCGTAGCCCCGTGTCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG  
 TGTACAACCGCCAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTATCTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA  
 CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCCGGGGAATCTACTGGGTGGTTGGAAATACT  
 CAAGTTTCTCTGGCTTCTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAGAAT  
 CCAGCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA  
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCACCCACCCACCCCCAGTTACC  
 CTCCAGCCACCTGCTGCATCTGTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
 AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCAGCTTCTCT  
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCCCAG  
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC  
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGGGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCTCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAACTGCTCCAC  
 CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTCCAGCTCTC  
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCTGAT  
 CTGTGCTGTCTTATTCTCTCCTTAGGCTTCTATTACCTGGGATTCCATGATTCATTCTCT  
 CAGACCCTCTCCTGCCAGTATGCTAAACCCTCCCTCTCTTTCTTATCCCGCTGTCCATT  
 GGCCAGCCTGGATGAATCTATCAATAAAACAAC TAGAGAATGGTGGTCACTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA  
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAAATTAAAAA

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## **FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32



**FIGURE 163**

[illegible]

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## **FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184  
><subunit 1 of 1, 388 aa, 1 stop  
><MW: 43831, pI: 9.64, NX(S/T): 3  
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGGRRS  
QWVRNWAVWRYFRDYFPPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLRREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSM  
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK  
HKTKFGLPETEVLEVN

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 76-97

#### **N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

#### **N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 165**

GGGCGGCGGGATGGGGGCGGGGGCGGGCGGGCGCCGACTCGCTGAGGCCCCGACGCGAGGGCGGGGCGGGCCCC  
 AGGGCCGAGGAGCGCGGCGGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCCCGCGCGACGAGCAGGTGG  
 CGGCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTT  
 GGACGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCCTGCTGGCCTTCCCTGAAGA  
 CCCAGTTCGTGCTGCACCTGCTGGTCCGGCTTGTCTTCTGTTGGTGAGTGGTCTGGTTCATCAACTTCGTCCAGCTG  
 TGCACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTG  
 GAGCCAACTGGTTCATGCTGCTGGAGTGGTGGTCTGACGGAGTGTAAGTGTTCACGGACCAGGCCACGGTAG  
 AGCGCTTTGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTTCGAGATCGACTTCCTCTGTGGGTGGACC  
 ATGTGTGAGCGCTTCGGAGTGTGAGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCCTCAT  
 CGGCTGGACGTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTTCG  
 AAGGGCTGAGGCGCTGTCCGACTACCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTCACG  
 GAGACCAAGCACCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCCTCAAGTACCACCTGCTGCC  
 GCGGACCAAGGGCTTCACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCTGA  
 ACTTCAGAGGAAACAAGAACCCGTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTG  
 AGGAGATTTCTCTGGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGA  
 GAAGGACGCGCTCCAGGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGAGGC  
 CGTGGACCTCCTGAACTTCCTGTCTGGGCCACCATTTCTCCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTC  
 TTTGCCAGCGGATCACCTCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAG  
 ACTGATAGGAGAATCGCTTGAACCTGGGAGGTGGAGATTGCACTGAGCTGAGATGGCATCACTGTACTCCAGCC  
 TAGGCAACAGAGCAAGACTCAGTCTCAAAAAAAAAAAAAAAAAACCCAGAAATCTGGAGTTGAACTG  
 TGTAGTTACTGACATGAAAAATTCAGTGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCT  
 TGAAGATGGTACCTTGAGATTTTTCAGGCTAATGAAAAAGAATGAAGGAAAAATTAACAGCCTCAGAGACCCAT  
 GGTGCACCGTCACACAAATCAACATATGCATGATGAGAGTCCAGAAAGGAGAGGAGAGAAAGGTCAGAAAGAA  
 TGGCCACAAGCTGATGAAAAACAGTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCA  
 GAGATCCACACCTAGATATTTCAATCAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCA  
 ACTTATCTTGTTCAAAGGATCTTTGATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGAT  
 AGTGGGATGAACACTGTTGAAGGCAAAACCTTCAACTGTAATTATTGGACTTTTGTAGTCTTAGATGGTCTGAC  
 CTCTTTGTCTTCAGGGACAGTTTTTCAATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAA  
 GGCCTGTCTTTAGGCCGGGCACAGTGGCTTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATC  
 ATTTGGGGTCAGGCTGATCTCAAACCTCCTGAGTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTGTGAT  
 TGCAGGCGTGAGCCACTGCGCTGGCCGGAATTTCTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTC  
 ACGCCTGTGATCCCAAGTAGCTTGGATTGTAAACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTAG  
 AGACGTGTTAGCCAGGCTGGTCTCGATCTCCTGACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGG  
 ATTACAGGCGTGAGCCACTGTGCTGGCCTTGAGCATCTTGTGATGTGCTTATTGGCCATTGTATATCTTCTA  
 TCTTCTTTGGGGAAATGTCTGTTCAAGTCCTTTGCCCTTTTAAATTTTTATTTATTTATTTATTTATTTG  
 AGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTACAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCT  
 GGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGTAGCTGTATTTTTTTGTATTTTGTATTTGTAGCTGTAG  
 TTTTTGTATTTTTTGTGGAGACAGCATTTACCATGATGCCAGGCTGGTCTTGAACCTCCTGAGCTCAAGTGAT  
 CTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGACATGAGCCACTGCACCTGGCAAACCTCCCAAATTC  
 ACACACACACAAAAAACCTGATTCAAATGGGCAGAGGGGCGGGTGTGGCCCCAACTACCAGGGAGAC  
 TGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTGCAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCC  
 TGGACAACAGAGTGAGACCCTGTCTC

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## **FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFVVFVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV  
MLLEWWSCTECTLFDTQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK  
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN  
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVQAASFGVRRLLIGESLEPGRWRLQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

**FIGURE 167**

GATATTCTTTATTTTTTAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTTCTCTTGTGCTTCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTTAAATGCTCTCATAAGACCACTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCACTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

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## **FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR

EGKINFYTNQDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS

GPCPPGQLHCTCGVLLSFL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAATACTGTTTTTTTGTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGTTA  
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTT  
CATAGGCGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGTGCCCGCCCCAT  
CTAACCTTTTCATGTCTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCCAAG  
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCAATCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAGGC  
ATCGAGTCTCCTGCATTGAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

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## **FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15



**FIGURE 171**

GCGGGCCCGGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCCTCCTGCCCCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT  
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCCAGCTCTTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC  
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
CTAGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282  
><subunit 1 of 1, 262 aa, 1 stop  
><MW: 28809, pI: 8.80, NX(S/T): 1  
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS  
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL  
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA  
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVVRVYIS  
LLPLGDGLTLAFKI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domains:**

amino acids 8-30, 109-130

#### **N-glycosylation site.**

amino acids 190-193

#### **Tyrosine kinase phosphorylation site.**

amino acids 238-246

#### **N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

#### **Amidation sites.**

amino acids 31-34, 39-42

**FIGURE 173**

CCGCCGCCGAGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCTGGGCCTCTCGCCGTCA  
 GCATGCCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCTCAC  
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCC  
 CATCTTTTCTTTGGCACACACGAAACAGCCTTCTTGGGACCCAAGGACCTGTTCCCTACG  
 ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAGGCTTCAATGAAGGGCTGTGG  
 GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCCCTCCGCCAGTGAGCTCCTCCGACAG  
 CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG  
 GGGTCATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC  
 GGTCTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT  
 GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAGAA  
 GCGCCGCTCAGCCTCCGACTCCGACTCCAAGGCCGATTCCGACGGGGCCAAGCCTGAGCCGG  
 TGGCCATGGCGCGGTCCGGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG  
 TCTGTGAAGAAGCCTCCGAGGGGCGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG  
 GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
 TGGACCGCATCAGTGAGTGGAAGCGGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCGG  
 CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA  
 GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGGCGGCAGCAGCGGGG  
 ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT  
 CCCCCGTCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC  
 GAAGAAGCCGCAGTCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG  
 TGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC  
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT  
 GCAGAACTGCACAGTGAGATCAAGTTTGCCCTAAAGGTCGACAGCCCGGACGTGAAGAGGT  
 GCCTGAATGCCCTAGAGGAGCTGGGAACCCTGCAGGTGACCTCTCAGATCCTCCAGAAGAAC  
 ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA  
 GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCCTCGGCCAAAGATCGAGGCCG  
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG  
 GAGCTGGCCGGGGAGGAGGCCCCCCCAGGAGAAGGCGGAGGACAAGCCAGCACCGATCTCTC  
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG  
 AGGAGGGTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC  
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACG  
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGCCGCGGGCAGCCAGGCCCAGCCCCGCG  
 CCGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGG  
 GAACGCTGTGCTGTTTGTATTGTTCCCTTGGGTTTTTTTTTCTGCCTAATTTCTGTGATT  
 TCCAACCAACATGAAATGACTATAAACGGTTTTTTAATGA

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## **FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIIDDIADGAVKPPPKNKYPIFFFFGTHETAFLGPKDLFPYD  
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRG  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDQFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEFPVKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAQKPVKVERTKRSEGFSDMRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC  
LNAL EELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEKLAG EELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE  
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

**FIGURE 175**

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATT  
 AACACCATTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAA  
 GATTTTCACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTTCTCCAGTCACTGGCACTTTGAA  
 GCAAAATATTTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTT  
 CATCAGAAGGACTGGATTTTCAAACCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGAC  
 CACATCTTTCTACTCAGTCTGGTTGACTTAAACAAAATTTTAAAGAGATTATTGGCCTGCTGCAAAGGAACG  
 GGTGGAATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCT  
 ATAACAAAACCTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTC  
 TACAAGGAGGATATTATATTCAAACCTAGACACACATAAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCC  
 TCAGCAGCCTTTTGTCTCAGTAATGACAGATGAGTACCTTACTCTGGAACAGCTTCTGATTTCCTTGGCAAAG  
 ATACTGCATTCACTCGATCCCTTGGGCCTACTCATGACCACCACTACATCAGAAGTACATTCAGAGCACTAC  
 TGGCTCAATGGAGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATA  
 TTTCTTCTTTCGTGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTCTCGAGTTGGAAGAGTTT  
 GTAAGAAATGATGTAGGAGGCAACGCAGCCTGATAAACAAAGTGGACGACTTTTCTTAAGGCCAGACTGATTGTC  
 TCAATTCCTGGAAGTATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTTACTCCCAAGAGA  
 TGAAGAAAATCCTGTAGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGT  
 ATAGCATGGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTG  
 CAGTATGATGGGAGAATTCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTC  
 CACCCGAGATTTTCCAGATGATGTATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATCCAG  
 TTGCAGGAGGACCAACGTTCAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCAATT  
 GCAGAAGATGGCCAGTACGATGTAATGTTTCTTGGAACAGACATTGGAACGTGCTTCAAAGTTGTGAGCATTTTC  
 AAAGGAAAAGTGAATATGGAAGAGGTAGTGTCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGA  
 ACATGGAATTGTCTCTGAAAGCAGCAACAATTTGATACATTGGTTCCCGAGATGGATTAGTTAGCTCTCTTGCAC  
 AGATGCGACACTTATGGGAAAGCTTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAAA  
 TGCATGCTCTCGATATGCTCCTACTTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGGCACCCCAATCA  
 CCCAGTGTGGGACATCGAAGACAGCATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAAATTT  
 AACTCAACCTTTCTGGAATGTATACCTAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGGA  
 TGAGCATCGAGAGGAGTTGAAGCCCGATGAAAGAATCATCAAAACCGAATATGGGCTACTGATTGGAAGTTTGC  
 AGAAGAAGGATTCTGGGATGTATTACTGCAAAGCCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACT  
 TTGAATGTCAATTGAGATGAAACAGATGGAAAATACCCAGAGGCGAGCATGAGGGGAGGCGAGGTCAAGGATCT  
 ATTGGCTGAGTCACGGTTGAGATACAAAGACTACATCCAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGT  
 ACTGCGAACAGATGTGGCACAGGGAGAAGCGGAGACAGAGAAACAAGGGGGGCCAAAGTGGGAAGCATGACG  
 GAAATGAAGAAGAAACGAAATCGAAGACATCACAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTT  
 TTCTACTTAATTTAAAGAAAAGAAATTCCTTACCTATAAAAACATTGCCTTCTGTTTGTATATCCCTTATAGTA  
 ATTCATAAATGCTTCCATGGAGTTTTTGCTAAGGCACAAGACAATAATCTGAATAAGACAATATGTGATGAATA  
 TAAGAAAGGGCAAAAATTCATTTGAACAGTTTTTCCAAGAACAATCTTGACAAGCAAAGTATAAGAATTAT  
 CCTAAAAATAGGGGGTTTTAGTTGTAATGTTTTATGTTTTGAGTTTGGAAATTTATTGTCTAGTAAATAGTT  
 GAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGTGCTTTATTCCTCGAATGTCCATTAGCATGGAATTT  
 ACCATGCAGTTGTGCTATGTTCTTATGAACAGATATATCATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGA  
 ATAAGAGGTGAGACACAAATTAAGACAACCTCCATTATCAACAGGAACCTTTCTCAGTGAGCCATTCACTCTTG  
 AGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTCTGGCCACTGGGGTTAAATTTAGTGACTACAACA  
 TTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCTATTGACTAGTCAGGAGTAACAGGTTTCACAGAGA  
 GAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAAGCTCTACAGGGACAGAATGCTTAATAAATACT  
 TTAATAAGATATGGGAAAATTTTAAATAAACAAAGGAAAACATAATGATGTATAATGTCATCCTGATGGGAAGG  
 CATGACGATGGGATTTGTTAGAAGACAGAAGGAAGCAAGCCATAAATCTGCTTTGGGGAAAACCTCATATCC  
 CCATGAAAAGGAAGAACAATCAAAATAAAGTGAGAGTAATGTAAATGGAGCTCTTTTCACTAGGGTATAAGTAG  
 CTGCCAATTTGTAATTCATCTGTAAAAAAAATCTAGATTATAACAACTGCTAGCAAAATCTGAGGAAACATA  
 AATTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTATAACCAATGATATTTCAGTATATATTTCTCTCT  
 CTTTTAAAAAATTTTATCATACTCTGTATATTATTTCTTTTTTACTGCCTTTATTTCTCTCTGTATATTGGATT  
 TTGTGATTATATTGAGTGAATAGGAGAAAACAATATATAACACACAGAGAATTAAGAAAATGACATTTCTGGG  
 GAGTGGGGATATATATTGTTGAATAACAGAACGAGTGTAATTTTAAACAACGGAAAGGGTTAAATTAACCTCT  
 TTGACATCTTCACTCAACCTTTTCTCATTTGCTGAGTTAATCTGTTGTAATTGTAGTATTGTTTTTGTAAATTTAA  
 CAATAAATAAGCCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYSKDLLLSNSCIPFL  
GSSEGLDFQTLTLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRCLKCPFD  
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNAGAKFIGTFF  
IPDTYNPDDDKIYFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQSRSLINKWTTFLKARLIC  
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP  
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV  
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSSISKEKWNMEEVLEE  
LQIFKHSSIIILNMEISLKQQQLYIGSRDGLVQLSLHRCDTYKACADCCLARDPYCAWDGNA  
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA  
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTILN  
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
KGGPKWKHMQEMKKRNRHRLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCCGCGGGGAGCAG  
 ACAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCC  
 ACCTCAGCAGTTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAGCGTGGCTGGCA  
 AGAGTGGCCTGGAGAAAGAGGTTTCAAGCTGTGACAGCCGAGCTGCCCGTGAATAAGATCCAGAACCATGGG  
 CATCGGGTGAGGTGGGGGGGACAGGTGTATGTGCACCTTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGGAT  
 CTTGGAGCCATTGAGGCTGTATGGAGCTACAGAGGGGAGGGAAGGTATTTAAGGTAACAGTGTGGCACAAT  
 AGTTAAGAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGCTTCCCTAGTTCTGTAGC  
 CCCAGGTAAGGGATGACTTAACCTCTCTGGACTTAATTTCTCATCACTAAAGTAGGGGCAATAATAGACC  
 CACCTCATAGGGAAGATTAAATGACATAATGTATGTATGCACTAGCAAAGTACCAGTCCCATAAGTCAAT  
 GCCCACAGTATTTCCACCCACCCCTGTTCTCTGCCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGG  
 CAGCAGGCTTCAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGAGCATCCGCCGGGC  
 ACAGGTGAGCCAGGTGAAGGGGGCTGCCGGCTGGCCCTGCTGCAAGGGGCTGGCTTAGATGTGGAGCGCTGGC  
 TGAAGCCAGCCATGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAG  
 AGGGACCTCTCTCCAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTT  
 TGAGGAGCCTGCCCCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGG  
 CAGGGCTTGAGGATGAGTGAACAATCACGGAGGTTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAA  
 TGGGTCAAGGCTCGGAACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTC  
 CCTCCAGAGAGCAGCCAAGACAGTGACAATCCCTGCCGGGCAGAGCCACAGCATTCCTGGCACAGGCCCTGT  
 ACAGCTACACCGGACAGAGTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGCTGCTGCCCCGGGC  
 CAAGATGGAGTAGATGACGGCTTCTGGAGGGGAGAATTGGGGGCCGTGTTGGGGCTTCCCTCCCTGCTGGT  
 GGAAGAGTGCTTGGCCCCCAGGGCCACCTGAACCTCTGACCTGAACAGATGCTGCCGTCCCTTCTCCTC  
 CCAGCTTCTCCCCACCTGCACCTACCTCTGTGTTGGATGGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCC  
 CTGGACTTCCCTGGGTCTCTGGACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGC  
 TAAAGCCCCGGATCCTGGCCACCCAGATCCCCCTACCTGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGC  
 TGTCCCTATCTTCAAGCTGTGAGACCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCT  
 TATTTCCACCTCACCTCCAAGGTTGGAACTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTT  
 CCCATTTCTATCATCTCTAGGACCGGAACCTACTACCTTCTCTTCTGTGTCATGACCCATCTAGGGTGGTGA  
 TGCCTGAAATCTCTGGGGCTGGAAACCATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCT  
 GGCTCCATGACCCACCCCACTCTGGATGCCAGGTCACCTGGGGTGGGGTGGGGAGAGGAACAGGCCCTTGGGA  
 TCAGGAGCTGGAGCCAGGATGCGAAGCAGCTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCAG  
 AAGGCCAGGCCAGGGCTTGGGCTCTTGTGCTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCCA  
 CCACGGGCAGGGGCTGCTCCAGCTGCCAGCTCTATCATATGAGCGAGGTGTTGGGAAGCGGGGCAGGC  
 AGCCTGTTGAGGAGGGGAAGGAGAAGAGACTGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTG  
 TGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTCAGCTGGGGGGCAGTGCTGTCCAGTGAGGGGAGGGCTTTCA  
 CGCCACCCACCCCTGGCCCTGCCAGCTGGTAGTCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAA  
 TAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGCTTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCA  
 CCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGCAGTTTACTCTGGGGTTTCAAGGAGCCGAAAGGCTTAA  
 TAGTTTAAGTAGGTGATGGGAAGATGAGATTACCTCATTAGGGCTCAGGCAGACTCACCTCACATACTCCCTG  
 CTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGGTCAACAATGAGAGACCAGGAGTAGGTCTATCAGTG  
 CCCCCAGAGTAGAGCAATAAGAGCCAGCCAGTGCAGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAA  
 GTGCTGGTTTTGCTTGGCTGCCATTGCTCTTGAAGGGCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCT  
 CAGTGTGGCTCTGCAGAGCTCTGGGGTTCCCTTCAAGTGCACGAGGGGTTAGGCTGTCTGCTGCTGAGTCCCT  
 CATTCTGTAAGTGGGGGCTGGCTAGGACCTGGGGCTGTGGCCTCTCAGGGGGCAGCCTCTCCATGGCAGGCATC  
 CCTGCCCTGGGGCTGCCCTCCCCAGACCCCTGACCAACCCCTGGGTCTGTCCCCACCAGAGCCCCAGCTCCT  
 GTCTGTGGGGAGCCATCAGGTGTTCGTGCAAGTGCATAGCGCTTCTCAATGTGTGTCACCCGGAACCTGGGAG  
 GGGAGGGAACACTGGGGTTTAGGACCAACAATCAGAGGCTGCTTGGCCCTCCCTCTGACAGGGACATCCTGA  
 GTTTGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTCAGATTGTGGGGCACATTGTGTAGCCTGA  
 CTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTTTTGGGATCAGGTGCCTGATCACTGGGC  
 CCCCTACTCGAGCCCCCTTCCCTGGAGCACCTGCCCACTGCCACAGAGAAACATAGTGTCTCCCTGTCTC  
 CGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAGGCTCTTGTGCGGCTGCAATGGAT  
 GCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTCCGTCTGCAGGTGGAGGTGGCAT  
 CCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTCCCTTCATGTTTTGTTTCTTACGTTCT  
 TTCAGCATGCTCTTAAACCCCAAGCCCCAATTTCCCAAGCCCCATTTTTCTTGTCTTATCTAATAAA  
 CTCATATTAAG

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## **FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEPPAPQALATRALPCPAHVVFQYQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSLPESQSDNPGAEPTAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPFELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPQDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT



**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGA  
AGAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCA  
GAAGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCC  
TGGGCACCTCTCCCAGCCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCCCTCAGCCCTTCTGAAAACCTT  
TGCCTCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGAC  
TTGGTGCCTTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCCAGACAGGCTCGCATCCCCG  
GAGGGGCTTGGCAGGGCGTGGCTGTGGGAGCCCCAACCTGCCTCCTGCTCCCCATTGTGCGCTCTCTGCG  
TGGTGTGGCTGCTTCTGCTACTGCTGGCTCTCTCCTCAGCCCGCTGGCCAGCCCCCTCCCCGGGAG  
GAGGAGATCGTGTTCAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCTGCCAGGCTGTTGTG  
CCGCTTGACGGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGA  
CAGTGCAGTACCTGGGCAGGCGCTGAGCTGCTGGTGAGCAGAGCTGGCACCTACCTGACTGGCACCATC  
AATGGAGATCCGGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGCGTGTACAAATATCGGGG  
GGCTGAACCTCCACCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTAC  
GCCGAAGAGTCTGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGA  
CCCCGAAGAGCCAAAGCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGAGATGACAAGATGGC  
CGCATTCACGGTGCAGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCCTTCAAGCACC  
CAAGCATCCGCAATCCTGTGAGCTTGGTGGTGAATCGGCTAGTGATCCTGGGGTCAAGCGAGGAGGGGCCCCAA  
GTGGGCCCAAGTGTGCCCCAGACCTGCGCAGCTTCTGCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTC  
GGGCCCTGACCACTTTGACACAGCCATTCTGTTTACCCGTGAGGACTGTGTGGAGCTCCAGTTCGCAACCGC  
TGGGTATGGCTGATGTGGGACCGCTCTGTGACCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAG  
TCAGCCTTCACTGCTGCTCATGAATGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGATCAG  
TTTTAATGGGCCCTTTGAGACCTCTCGCCATGTCATGGCCCCCTGTGATGGCTCATGTGATCCTGAGGAGCCCT  
GGTCCCCCTGCAGTGCCCGCTTTCATCACTGACTTCTCTGGACAATGGCTATGGGCACTGTCTCTTAGACAACCA  
GAGGCTCCATTGCATCTGCCTGTGACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTT  
CGGGCCCCGACTCAGCCATTGTCCACAGCTGCCGCCGCCCTGTGCTGCCCTCTGGTGTCTTGCCCACTCAATG  
GCCATGCCATGTGCCAGACCAAACTCGCCCTGGGCCGATGGCACACCCCTCGGGCCCCGACAGGCCTGCATG  
GGTGGTGCCTGCCTCCACATGGACAGCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGGTCTTGGGG  
ACCATGGGGTGAATGCTCTCGGACCTGTGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCCTGTCC  
CCCCGAATGGTGGCAAGTACTGTAGGGCCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCACT  
GGCTCAGCCCTGACCTTCCGCGAGGAGCAGTGTGCTGCCTACAACACCCGACCCGACCTCTTCAAGAGCTTCCC  
AGGGCCCATGGAAGTGGGTTCTCGCTACACAGGCGTGGCCCCCAGGACCACTGCAAACTCACCTGCCAGGCCC  
GGGCACTGGGCTACTACTATGTGCTGGAGCCAGGGTGGTAGATGGGACCCCTGTTTCCCCGAGCAGCTCCTCG  
GTCTGTGTCCAGGCCCCGATCCATGCTGGCTGTGATCGCATCATTGGCTCCAAGAAGAAGTTTGACAAGTGT  
CATGGTGTGCGGAGGGGACGGTCTGGTGTGACGACAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACA  
ACAATGTGGTCACTATCCCCCGGGGGGCCACCCACATTCTGTCCGGCAGCAGGGAAACCTTGGCCACCGGAGC  
ATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTATGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCAC  
AGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTACAGCGGGGCCACTGCAGCCTCAGAGACATGTCCAGGCC  
ATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTAGTGGCTGGCAACCCCCAGGACACACGCCTCCGATAC  
AGCTTCTTCTGTGCCCGGGCCGACCCCTTCAACGCCACGCCCCACTCCCCAGGACTGGCTGCACCGAAGAGACA  
GATTCTGGAGATCCTTTCGGCGGCGCCCCCTGGGCGGACAGGAAATTAACCTCACTATCCCCGCTGCCCTTTCTGGG  
CACCAGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTTCTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAG  
GGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAATGCGCAGGCTGGCCCTGCCCTGGTTCCTGCCCT  
GGGAGGCACTGATGGGTTAGTGGATGGAAGGGGCTGACAGACAGCCCTCCATCTAAACTGCCCCCTCTGCCCTG  
CGGGTACAGGAGGGAGGGGGAAGGCAGGAGGGCTGGGCCCCAGTTGTATTTAGTATTTATTTACTTT  
TATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAACCTGACCCCTGACCCCTCATAGCCCTCACC  
CTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTGTGTGTATGCGTGTGTGTGTGTGTGAAA  
ATGTGTGTGTCTATGTATGAGGTACAACCTGTTCTGCTTTCCTCTCTCTGAATTTTATTTTGGGAAAAGA  
AAAGTCAAGGTAGGGTGGGCTTCAAGGAGTGAGGATATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
TTTTTTTGGAGACAGAATCTCGCTCTGTGCGCCAGGCTGGAGTGCAATGGCACAATCTCGGCTCACTGCATCCTC  
CGCCTCCCGGGTTCAAGTGATTTCTCATGCTCAGCCTCCTGAGTAGCTGGGATTACAGGCTCCTGCCACCACGC  
CCAGCTAATTTTTGTTTTGTTTTGTTTTGTTTTGAGACAGAGTCTCGCTATTGTACCAGGGCTGGAATGATTTCACT  
CACTGCAACCTTCGCCACCTGGGTTCCAGCAATTCTCCTGCCCTCAGCCTCCCGAGTGTAGATTATAGGCAC  
CTACCACCACGCCCCGCTAATTTTTGTATTTTTAGTAGAGACGGGTTTTACCATGTTGGCCAGGCTGGTCTCG  
AATCCTCTGACTTAGGTGATCCACTCGCCTTATCTCCCAAAGTGTGGGATTACAGCGTGTAGCCACCGTGCC  
TGGCCACGCCCAACTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTACCAATGTTGGCCAGGCTGCTCTGAAC  
TCTGACCTCAGGTAATCGACCTGCCTCGGCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACCCAGCCCGG  
TACATATTTTTTAAATTGAATTCTACTATTTATGTGATCCTTTTGGAGTCAGACAG

**FIGURE 179B**

[illegible]

**FIGURE 180**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNQSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHLRRKSP
ASGQGPMCNVKAPLGSPSPRRRAKRFAASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCCLHMDQLQDFNI PQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
LTCQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFKDKMVC GG DG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRISIYALKLDPGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRRAQILEILRRRPWAGRK
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152,  
167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560,  
577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
AATTGTCTGTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY  
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT  
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI  
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY  
TENGIEFDPMLEDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV  
ARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38,, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA  
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
GGCACCCCTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGCC  
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLTITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLLCLSCQ  
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

**FIGURE 185**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCT  
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCCTTTGTGCAATTGCTGGAGT  
GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
GCATGGGTGGGATGGTGCAGACTGTTCAAGACCAGGTACACATTTGGTGGCGCTCTGTTCGTG  
GGCTGGGTGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTTCTTATCATGCCTCAGGCCACAGTGTTG  
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
ATATACGATGGAGGTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCAGCTA  
TGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA  
AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGAATCACAGCTGGAAGTTAGAAAAGC  
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA  
TTTCCCAGCTTATCCCCAAGAAAACTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
TGATCTTAAAAGTTACCAAACCAAAGTCATTTTTCAGTTTGAGGCAACCAAACCTTTCTACTG  
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG  
TCCTCTTTCTGTGCGGGTGCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT  
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC  
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
GGCAACATGGAGAAAGCCCTGTCTCTACAAATAACAGAGAGAAAAAATCAGCCAGTCATGGTG  
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
AGGTTGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGA  
TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA  
ACTAATTCTTTAA



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## **FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG  
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGG  
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTC  
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC  
CATGCAAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA  
CTGTTCTTAACCTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG  
AAGAAGGTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA  
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT  
TTCTTGTTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGCTTTGCAATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAACA  
ACAAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
TCATTTTGTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTTAGTTTTACTAAA  
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA  
AAGTTTGTGTGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA  
TTAATAAATTGTACATTTTTTCTAATT

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## **FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTGTCATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT  
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCCGCTACTCAACATCTGCCCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTTGAAGTATTTAAAAATTCATTT  
GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTCACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCCACCTCCGGAACCTCTGACCTCTGTTTCCTCCGTCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCCTCGTCTCACCCCTTTTAACTCACATTTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

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## **FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPHSHMARYSTSAPAISRGPSYPTKNYV
```

### **Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC  
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACCTTCAGGAGTCCTCTTCATCCTGAC  
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT  
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAAAACATATACCTATTCTA

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## **FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSSTSYV

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA



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## **FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTT CAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

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## **FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL

GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDIYQRHYD

EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTTACAGCAACACCGCCAG  
CCCCGGACTCCCCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCTCAATGATTGAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG  
GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCTGCCC GCCGGGGTCCGAGCCCCGCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCCATGTACCGCCCCTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC  
GGACCTTGCTCCCCGCGCCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCCGA  
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCGCTTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA  
AAAAAAA

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## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCCCTCCAAGGATGACAAAAGGCGCTACTCATCTATTTGGTCAGCAGC  
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGACAGGCATCCACTGCGCAAAAAGGA  
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTGACCGTGG  
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA  
CTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAAACCTGACCAGAGCCCCAGGAATAAA  
TGGTTTTCTTGGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
 CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
 TTGGGGTGAAACTTGGGTCTGTGGT'TTCTGATTGTAAGTGGAAGCAGGTCTTGACACACGC  
 TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTTGATGATGGTGGCGATGT  
 TGCACCTCCCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCCAGCTGGACCCAC  
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG  
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
 CCAGGGCCTTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCCGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCCCTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTTGGACTGGAAGCTGGATTTCCTACTGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCCTGTG  
 GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCTCAT  
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTGTGCGACATTCCACTGG  
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT  
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTGAGGCAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
 AGAATGGGATGATTGTCCACATTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC  
 AATAAAGATTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA  
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGTAAGGAAAAGAGAATTTTGCCATC  
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA



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## **FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRRTVHSILDTPPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVSP  
VIDVIDWKTFQYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLLGCRTFHWFLANVPPEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCCCTCCCACCGCTGCTCAGGGCTTTTCATCCTCCCCTCGAACCCACCAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG  
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTGACAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATTCT  
 CTGTTCTGGGGGCCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT  
 CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCTTCGGGGACTCACCTACCCCCACCC  
 TGACCATGAGGAGCCCCGAGGGGGACCCGGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTCCAGTTGAACCGGTGAGGGGCAGGGGCAATGGGATGGGAGGGCAAGAGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
 CTCCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATTCTCTGCTGCCATAACTCCAACCTCTGCCC  
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCTTCTATTCTGGCCTACCCCTTGTTTCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCCTTGGTGAATCTGTGATGCCCCAATGTTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCGGAACACTCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC  
 AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATAACGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGCAACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGG  
 TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCATGG  
 TCTCGTCCCATTCACACCAATTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA  
 CTGCTAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG  
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT  
 CCCTTTGGGGCTCCCTAACTCCACCTAGGCTGCCAGGGACCGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTCTGCCCTCAAGTCTACCCCTCCCTTCCCGGACTCCCTCCTGTCCCCCTCCTTT  
 CCTCCCTCCTTCTTCCACTCTCCTTCTTTTGGCTTCCCTGCCCTTTCCCCCTCCTCAGGTT  
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTCCTTCCCTTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATTATCTCTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

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## **FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCCGCGCTGCCCTCACTCCCGGCCAGGATGG  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGCGCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCCGCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

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## **FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

><subunit 1 of 1, 121 aa, 1 stop

><MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG  
PPAPTVPAGPEDSTAQERLDQGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCC  
CCAGAGGCGCTGGGAGTGTGGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
CGACTGTGACACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG  
ACTCGCACGTCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC  
CTGGCTGTGTCATCGGCTAGGGCGGGGCCGTGGGTTTCAGGGGCGCACCACTTCCAAGCCTGTGT  
CCCACAGGTCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC  
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCCTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTCTAAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTGCCTTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

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## **FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

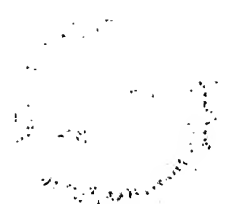
><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

**FIGURE 209**

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT  
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC  
ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
TAGCATGGTGCAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAAC TG  
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG  
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAAC TG  
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAAC TAAAGGAGTCTCAACTGCCAG  
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAAGTTTCC  
GTAGAGCATGTGCAAACTTTTGTGATGGATTCC TAAAGTGGAATAATTGTTGAAAGAAAATCG  
TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC TTGACTTCTCCTTGGAACTACATATGGCC  
AAGTATCTACTTTATGCAAAGTAAAAAGGCACAAC TCAAATCTCAGAGACACTAAACAACAG  
GATCACTAGGCCTGCCAACACACACACACACGACGTGCACACACGCACGCACGCGTGACAC  
ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC  
TTCTTCCTTCTTTTAAATTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
CCTCTATGAAAGAGAGGCATTCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGT  
TTGTATACTGCACATGACTTACACACAACATAGTTCTGTCTTTTAAAGGTTACCTAAGGGT  
TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
CCTGAACTCAGCAGAAATAGACCATGTGAAAAC TCCATGCTTGGTTAGCATCTCCAAC TCCC  
TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA



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## **FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQKGILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVEHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGAGGTGCCACCCGGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGCGGCGGCGGCGGCGGACTGCAGTGGCTGGACG**ATGGC**AGCGTCCGCCGGAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCCGGTGCTGGCGGCGGCGCTTGG  
GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC  
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
TATATCTGTGATGTCAAAAACCTCCTGCATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCAGGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAAG**AGAATACCTAGAACATATC  
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA  
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC  
AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCCTTTCCACATCATTTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACT  
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
AAATGTGTCATATCAATTTCTGGATTCAATAAGCAAGATTAGCAAAGGATAAATGCCGAAG  
GTCACCTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT  
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTA

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## **FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCTSESLSQVQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGA CTGCCCGGGCTGCCGCC  
CCCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGGCTGCCGCC  
TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
TGGCAGGTGGGCTGAGGGGCGCGCCCCGGCGCAGTCCCCCGCGGGCCCCGACCCTGAGGCG  
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
TGGTCAGAAGGTTTTAGGTTATGCTGATGTTGAGAACCGTG TACCATGTAAACCAGAGACAGT  
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA  
TATGAAGGTGAAAAGGTTTCTGT CACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCTG  
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCCAAAAGTAATGAAAAGAATGATTTT  
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA  
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTC AATTGAAT  
CCCTAAGATTATTTAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
CAGTGATTTACAATAGAGCAAGGTTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
TTAACACTATTTTATTAATTA AAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAAACA  
TGTTTATAAAGTAAAAAAA

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## **FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWGGLGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTGCGATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT  
GGTGC GCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
TGGAGTCGCACCTGTGCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCCTGTTCTCATGATGTCAGG  
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG  
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTTCAGAAACCCAAG  
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

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## **FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEA  
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGGSGLCCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGAGCAGGTCGTCCGGGGGCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA  
ACTGCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
GCAAGAATTCTTGTGTCTCTCTCCCTGACTTACTCACTATGCTGCTTAACCAA  
ACTCTCTCAAGACTACTTTGTGTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC  
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCCTCATAGCCTTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAGCATTTGCTCTG  
CTGTATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT  
GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA  
ATAAACACTTTTAAATGATCAAAAAAAAAA



## **FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET  
EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFICSAMVMALLAVVGLFTVVRHDA  
ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATG  
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA  
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
TGGTAGAAAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGA  
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनावदन्स  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

[illegible]

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## **FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPTYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDL SQRYCLMAVFNVIIYLENEDSE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTGCGTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

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## **FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK

LGDSWDVKLGALGCNTQEVTLQPGEYITKVVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAACTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTTCTTGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTTTCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTATGCAACTGGCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAAATTACAGGAGATACCTTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAAATTTACGGAACCTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
 TGGAACCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAACTTACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGTCATAG  
 GACAGACCATGCTTGGACCTGGAGCTCCTTACAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTG  
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACCTC  
 TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG  
 CAAGATCCTTCCCTGTCCGTTTTAGTGCAATTCATAATACTGGTCATTTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGGTTTAAATATAA  
 TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTGTTTTAAGATAAACT  
 TCTTTCATAGGTAAAAA



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## **FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTVELLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG  
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF  
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL  
DLGYNRIRSLARNVFAFMIRLKEHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTM  
SWTWSSLQRLDLGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA  
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLA  
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI  
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN  
GTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAACCCTATCCTAAGTTGACTGTCCTT  
TAAATATGTCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATAA  
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGAGGAGCTCAGGGCTTG  
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
AAACATCAATAGATATCTAAAAA

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## **FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
ACGCCAGCTCAGTTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT  
CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC  
TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTTA  
CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGATTTGGACTCATT  
TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA  
ACACAGTGGATGTGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC  
TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAAGCTTTATAATTGCTGGCTTAGGAC  
AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC  
TCTAATTCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTTTCAAGCAAGTCTGTTCAATG  
CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC  
ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA  
TCATTCTGTCTATTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTG  
CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAATATAATGTTGAAAA  
TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA  
AGGTAAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT  
GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA  
AAGTATTCATGATTTTTTACATACATGAATGTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCT  
ATGCTATCAGGAAAGCACATTATTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC  
TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA  
GGTACTTTTGTGCTGCATTAAATTGCTTGGAAGTGTAAACATTATATTATATAAGAGTATC  
CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
TAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAAGGAAAAAAGCT  
GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT  
TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT  
CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAATA  
TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTTCTCTCTCTGTA  
CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

**FIGURE 230**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL  
VPVTTNKRTNVSGSIR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGCCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCCGTGGCCCCCTGCTGCTGCTGCTGCGCGTGAGTGGGGCCCAGACAACCCGGCCATGCT  
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCCTTTTCGACAGCTTCAGCCTGACTCGG  
GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCCA  
CTTGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT  
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCACCTGCC  
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG  
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
CACAACCTCATTACCCGCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCCACCAT  
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC  
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG  
CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGACCTGTGCGGCAACCCCAAGCTTAAC  
GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
AACCTGGTGCCCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT  
CCAGCCCCAAGGTGCCCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  
ATCTTGT**GACA**CAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCTCAG  
GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCAAGTGGGGAGCCCCGAGGCCTATGTGGCA  
GCGTCACCACAGAGATTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCCTCCCTCAT  
GCCTGGGCCCGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
GTTCAGGTCCACTGGGCTGAGTGTCCCCTTGGGCCCCATGGCCCAGTCACTCAGGGGCGAGTT  
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC  
AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCTGCGGGCAGTGGC  
ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCCGACCCAATGCACTTTCTTGTCTCCTCTA  
ATAAGCCCCACCCTCCCCGCCTGGGCTCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA  
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
CCAGCCTAGCCAGTTTCTCACCCCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC  
CATTTTCCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
TCTGGCTGGGATCTCCAAGGGGCCCTCCTGGATTGAGTCCCCACTGGCCCTGAGCACGACAGC  
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC  
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTCCCTTAGTCTTCATTTTA  
TAAAGTTGTTGCCCTTTTTTAACGGAGTGTCACTTTCAACCGGCCCTCCCTACCCCTGTGGC  
CGGGGATGGAGACATGTCAATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAT  
ATTGTCTCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC  
CCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGGTTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS  
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC  
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC  
TCTAGTCTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC  
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC  
TGCAATGGATGGAGGAGACAGAATTAGGAGGAAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTT  
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGTCTATTTAATGTATTT  
ATTTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
AGCAGGTGATGTATTTTTTATACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCT  
AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
CCAAAAAAAAAAAAAAAAAAAA



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## **FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSTLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAADVVKALG  
ELDILLQWMEETE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAAATCTGCCCCCTATAGGGGAATGGTGCGCACA  
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTTTGGCAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAAGTGCAAAT  
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGATTTCTGTGGTGTACATCATGCATTTG  
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGT  
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTTTAA

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## **FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA  
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFVGKSEDEH  
YPLWKSIVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAAATGCACCTTA  
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT  
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTATTGTCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTTATTCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAAGTTTTTCAAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA  
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC  
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCTCTAATATGACTTTATGTGAGAA

## **FIGURE 238**

' MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCCA  
CTGGCGGCCCCGCAACACTCCGTCTCACCCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT  
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  
GATGAGAGTGTCAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
TGTTTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
GCCTCGCCCACCAAGGAGATCCAGGTAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGCTGGTGG  
CCTCCTACGACGATCCAGGGACCAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG  
GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
CCTCAGGGGTAAAGCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG  
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTTAGGGTGGC  
TGTGGCTCTTCCTCAGCCAGGGCCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCC  
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGACGC  
TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCACAGCACATCCTACCCGGAAGACC  
AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTGAGGG  
ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
TTTTTGCTGGTTTTTGAIAAAAAAAAAAAAAAAAAA

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## **FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
GCAAGAGAAGCAGAGATAAATACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTC  
TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTTCCAGTCCC  
CTGCACCCCTTCCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC  
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA  
GCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG  
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAAGCCACATTTGCAGAGCTCCACATTGTAC  
ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT  
GTCTTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA  
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA  
AGAGTGTGGTCTTCACCTCAGCACAAAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA  
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCCTGGACATCTCTTAGAGAG  
GAATGGACCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG  
GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA  
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA  
TATTTGGAAATTAAAGTTTCTGACTTT



**FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812  
><subunit 1 of 1, 337 aa, 1 stop  
><MW: 37668, pI: 6.27, NX(S/T): 1  
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWHPASYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ  
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT  
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

[illegible]

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## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTTLSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCCTCCAGTCCGCGCTGCCCG  
GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGACCTGTATAATGGAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG  
GAGTCCTGGACACCCAACCTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAATA  
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT  
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT  
AAAAATTATTTCCAACA

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## **FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217